

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: January 26, 2005, 11:30:01 ; Search time 24.6 Seconds
(without alignment)
520.089 Million cell updates/sec

Title: US-10-085-612A-1

Perfect score: 18

Sequence: 1 gacaaaggcagcagacag 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.4	91.1	29	US-09-144-367-13	Sequence 13, Appl
2	16.4	91.1	1345	US-09-372-339-2	Sequence 2, Appl
3	15.4	85.6	19	US-09-144-367-3	Sequence 3, Appl
4	15.4	85.6	4	US-09-144-367-4	Sequence 4, Appl
5	15.4	85.6	3	US-09-144-367-6	Sequence 6, Appl
6	14.8	82.2	32	US-09-144-367-12	Sequence 12, Appl
7	14.8	82.2	459	US-09-621-976-3153	Sequence 3153, Ap
8	14.8	82.2	807	US-08-154-019-28	Sequence 28, Appl
9	14.8	82.2	807	US-08-461-333-28	Sequence 28, Appl
10	14.8	82.2	807	US-08-464-167-28	Sequence 28, Appl
11	14.8	82.2	807	US-09-158-313-28	Sequence 28, Appl
12	14.8	82.2	807	US-08-476-798-28	Sequence 28, Appl
13	14.8	82.2	824	US-08-154-019-29	Sequence 29, Appl
14	14.8	82.2	824	US-08-461-333-29	Sequence 29, Appl
15	14.8	82.2	824	US-08-464-167-29	Sequence 29, Appl
16	14.8	82.2	824	US-09-158-313-29	Sequence 29, Appl
17	14.8	82.2	824	US-08-476-798-29	Sequence 29, Appl
18	14.8	82.2	1057	US-09-716-129-16	Sequence 16, Appl
19	14.8	82.2	1202	US-09-904-615-63	Sequence 63, Appl
20	14.8	82.2	1345	US-09-372-339-1	Sequence 1, Appl
21	14.8	82.2	1452	US-09-904-615-34	Sequence 34, Appl
22	14.8	82.2	1950	US-09-205-258-131	Sequence 131, App
23	14.8	82.2	4523	US-09-472-716-1	Sequence 1, Appl
24	14.8	82.2	4523	US-10-175-158-1	Sequence 1, Appl
25	14.8	82.2	6763	US-08-756-506-23	Sequence 23, Appl
26	14.8	82.2	10807	US-08-206-176-7	Sequence 7, Appl
27	14.8	82.2	10807	US-08-756-506-5	Sequence 5, Appl

28	14.8	82.2	16063	US-09-801-052-3	Sequence 3, Appl
29	14.8	82.2	16063	US-10-020-121-3	Sequence 3, Appl
30	14.8	82.2	29629	US-09-729-995-3	Sequence 3, Appl
31	14.8	82.2	29629	US-10-135-689-3	Sequence 3, Appl
32	14.8	82.2	48974	US-08-920-422-17	Sequence 17, Appl
33	14.8	82.2	66933	US-09-544-398B-11	Sequence 11, Appl
34	14.8	82.2	66933	US-09-543-771-11	Sequence 11, Appl
35	14.8	82.2	72049	US-09-544-398B-9	Sequence 9, Appl
36	14.8	82.2	72049	US-09-543-771-9	Sequence 9, Appl
37	14.8	82.2	118999	US-09-791-105B-32	Sequence 32, Appl
38	14.8	82.2	152331	US-09-128-155-16	Sequence 16, Appl
39	14.8	82.2	176373	US-09-128-155-17	Sequence 17, Appl
40	14.8	82.2	193303	US-09-497-855A-37	Sequence 37, Appl
41	14.8	82.2	193303	US-09-497-855A-44	Sequence 44, Appl
42	14.4	80.0	19	US-09-177-359-37	Sequence 37, Appl
43	14.4	80.0	420	US-09-702-705-1114	Sequence 1114, Ap
44	14.4	80.0	420	US-09-736-457-1114	Sequence 1114, Ap
45	14.4	80.0	420	US-09-614-124B-1114	Sequence 1114, Ap

ALIGNMENTS

RESULT 1
US-09-144-367-13/C
Sequence 13, Application US/09144367
Parent No. 6432639
GENERAL INFORMATION:
APPLICANT: Lichner, Jay
TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
FILE REFERENCE: SEO-12P
CURRENT APPLICATION NUMBER: US/09/144,367
CURRENT FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/058,612
PRIOR FILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 29
TYPE: DNA
ORGANISM: H. sapiens
US-09-144-367-13

Query Match 91.1%; Score 16.4; DB 4; Length 29;
Best local Similarity 94.4%; Pred. No. 41;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 24 GACAAAGGCAGACAGAG 7

RESULT 2
US-09-372-339-2
Sequence 2, Application US/09372339
Parent No. 6174684
GENERAL INFORMATION:
APPLICANT: Rebbeck, Timothy
TITLE OF INVENTION: CYP3A4 NFE Variant and Methods of Use Therefor
FILE REFERENCE: PENN-0695
CURRENT APPLICATION NUMBER: US/09/372,339
CURRENT FILING DATE: 1999-08-11
EARLIER APPLICATION NUMBER: 60/096,586
EARLIER FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1345
TYPE: DNA
ORGANISM: Homo sapiens
US-09-372-339-2

Query Match 91.1%; Score 16.4; DB 3; Length 1345;
Best Local Similarity 94.4%; Pred. No. 58;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GACAAGGCGACAGACAG 18
DB 806 GACAAGGCGACAGACAG 823

RESULT 3

US-09-144-367-3
; Sequence 3, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq For Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0)...(0)
US-09-144-367-3

Query Match 88.9%; Score 16; DB 4; Length 1345;
Best Local Similarity 88.9%; Pred. No. 89;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GACAAGGCGACAGACAG 18
DB 806 GACAAGGCGACAGACAG 823

RESULT 4

US-09-144-367-44
; Sequence 44, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 19
; TYPE: DNA
; ORGANISM: H. sapiens
US-09-144-367-44

Query Match 85.6%; Score 15.4; DB 4; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACAAGGCGACAGACAG 18
DB 1 ACAAGGCGACAGACAG 17

RESULT 5
US-09-146-053-6
; Sequence 6, Application US/09146053A
; Patent No. 6399349
; GENERAL INFORMATION:
; APPLICANT: Ryan, James W.
; APPLICANT: Sprinkle, Terry Joe Curtis
; APPLICANT: Venema, Richard C.
; TITLE OF INVENTION: Human Aminopeptidase P Gene
; FILE REFERENCE: MCG103
; CURRENT APPLICATION NUMBER: US/09/146,053A
; CURRENT FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/057,854
; EARLIER FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 45546
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-146-053-6

Query Match 85.6%; Score 15.4; DB 3; Length 45546;
Best Local Similarity 94.1%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GACAAGGCGACAGACA 17
DB 565 GACAAGGCGACAGACA 581

RESULT 6

US-09-144-367-12/c
; Sequence 12, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 32
; TYPE: DNA
; ORGANISM: H. sapiens
US-09-144-367-12

Query Match 82.2%; Score 14.8; DB 4; Length 32;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACAAGGCGACAGACA 18
DB 27 GACAAGGCGACAGACA 10

RESULT 7

US-09-621-976-3153
; Sequence 3153, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO: 3153
LENGTH: 459
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 150..329
US-09-621-976-3153

Query Match 82.2%; Score 14.8; DB 4; Length 459;
Best Local Similarity 88.9%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACACGGCGACGACGAG 18
DB 198 GACACGGCGCTGACGACGAG 215

RESULT 8
US-08-154-019-28/c
Sequence 28, Application US/08154019
Patent No. 5633076
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/154,019
FILING DATE: 16-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,333
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:
LENGTH: 807 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-154-019-28

Query Match 82.2%; Score 14.8; DB 1; Length 807;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACACGGCGACGACGAG 18
DB 411 GACACGACGAGTCGACGAG 394

RESULT 9
US-08-461-333-28/c
Sequence 28, Application US/08461333
Patent No. 5741957
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,333
FILING DATE: 05-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)
US-08-461-333-28

Query Match 82.2%; Score 14.8; DB 1; Length 807;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACAAAGGCGACAGCAGAG 18
Db 411 GACAAGGACAGCTCAGAG 394

RESULT 10
US-08-464-167-28/c
; Sequence 28, Application US/08464167
; Patent No. 6013857

GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,167
FILING DATE: 05-JUN-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989

ATTORNEY/AGENT INFORMATION:

NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505

REFERENCE/DOCKET NUMBER: 16994-003124

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-543-9600

TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 807 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-464-167-28

Query Match 82.2%; Score 14.8; DB 3; Length 807;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACAAAGGCGACAGCAGAG 18
Db 411 GACAAGGACAGCTCAGAG 394

Query Match 82.2%; Score 14.8; DB 3; Length 807;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACAAAGGCGACAGCAGAG 18
Db 411 GACAAGGACAGCTCAGAG 394

RESULT 11
US-09-158-313-28/c
; Sequence 28, Application US/09158313
; Patent No. 6066725

GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,313
FILING DATE: 08/476,798

CLASSIFICATION: 08/476,798

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989

ATTORNEY/AGENT INFORMATION:

NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505

REFERENCE/DOCKET NUMBER: 16994-003125

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-543-9600

TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 807 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-158-313-28

Query Match 82.2%; Score 14.8; DB 3; Length 807;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACAAAGGCGACAGCAGAG 18
Db 411 GACAAGGACAGCTCAGAG 394

Query Match 82.2%; Score 14.8; DB 3; Length 807;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACAAAGGCGACAGCAGAG 18
Db 411 GACAAGGACAGCTCAGAG 394

Query Match 82.2%; Score 14.8; DB 3; Length 807;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 12
US-08-476-798-28/C
Sequence 28, Application US/08476798
Patent No. 6140552
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
by Bovine Species and Transgenic Methods
TITLE OF INVENTION: 38
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,798
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschultz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-476-798-28

Query Match 82.2%; Score 14.8; DB 3; Length 807;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACAAGGCGACGACGAG 18
|||||
Db 411 GACAAGGCGACGTCGAG 394

RESULT 13
US-08-154-019-29/C
Sequence 29, Application US/08154019

Patent No. 5633076
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
by Bovine Species and Transgenic Methods
TITLE OF INVENTION: 38
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/154,019
FILING DATE: 16-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,333
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschultz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 824 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-154-019-29

Query Match 82.2%; Score 14.8; DB 1; Length 824;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACAAGGCGACGACGAG 18
|||||
Db 417 GACAAGGCGACGTCGAG 400

RESULT 14
US-08-461-333-29/C
Sequence 29, Application US/08461333
Patent No. 5741957
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.

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; APPLICANT: Strijker, Rein
; APPLICANT: Heyneker, Herbert J.
; APPLICANT: Platenburg, Gerald
; APPLICANT: Lee, Sang He
; APPLICANT: Pieper, Frank
; APPLICANT: Krimpenfort, Paul J.A.
; TITLE OF INVENTION: Production of Recombinant Polypeptides
; TITLE OF INVENTION: by Bovine Species and Transgenic Methods
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,333
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,788
; FILING DATE: 15-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/895,956
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/619,131
; FILING DATE: 27-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/444,745
; FILING DATE: 01-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschultz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16994-003123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 824 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-461-333-29

Query Match      82.2%; Score 14.8; DB 1; Length 824;
Best Local Similarity 86.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GACAAGGACGACGAG 18
Db      417 GACAAGGACGAGTCAGAG 400

RESULT 15
; US-08-464-167-29/c
; Sequence 29, Application US/08464167
; Patent No. 6013857
; GENERAL INFORMATION:
; APPLICANT: Deboer, Herman A.
; APPLICANT: Strijker, Rein
; APPLICANT: Heyneker, Herbert J.
; APPLICANT: Platenburg, Gerald
; APPLICANT: Lee, Sang He
; APPLICANT: Pieper, Frank
```

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; APPLICANT: Krimpenfort, Paul J.A.
; TITLE OF INVENTION: Production of Recombinant Polypeptides
; TITLE OF INVENTION: by Bovine Species and Transgenic Methods
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,167
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,788
; FILING DATE: 15-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/895,956
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/619,131
; FILING DATE: 27-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/444,745
; FILING DATE: 01-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschultz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16994-003124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 824 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-464-167-29

Query Match      82.2%; Score 14.8; DB 3; Length 824;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GACAAGGACGACGAG 18
Db      417 GACAAGGACGAGTCAGAG 400
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Search completed: January 26, 2005, 13:15:19
Job time : 25.725 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 13:15:32 ; Search time 127.6 Seconds
(without alignments)
810.549 Million cell updates/sec

Title: US-10-085-612A-1

Perfect score: 18

Sequence: 1 gacaaaggcagcagacag 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 287294193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	14	US-10-085-612-1
2	16.4	91.1	229	14	US-10-146-575-13
3	16.4	91.1	529	13	US-10-027-632-106890
4	16.4	91.1	529	13	US-10-027-632-106890
5	16.4	91.1	714	13	US-10-027-632-25159
6	16.4	91.1	714	14	US-10-027-632-25159
7	16.4	91.1	1530	14	US-10-198-846-10454
8	16.4	91.1	24295	17	US-10-317-277A-4
9	16.4	91.1	25543	13	US-10-087-192-805
10	16.4	91.1	34455	13	US-10-087-192-1915
11	16.4	91.1	71251	13	US-10-087-192-355
12	16.4	91.1	73771	13	US-10-087-192-1636

13	16.4	91.1	119596	14	US-10-270-336-3	Sequence 3, Appl1
14	16.4	91.1	172637	9	US-09-805-458A-3	Sequence 3, Appl1
15	16.4	91.1	237961	6	US-10-433-580-2	Sequence 2, Appl1
16	16	88.9	41	16	US-10-035-833A-1329	Sequence 1329, Ap
17	16	88.9	41	16	US-10-035-833A-7586	Sequence 7586, Ap
18	16	88.9	339	18	US-10-425-115-69563	Sequence 69563, A
19	16	88.9	745	15	US-10-027-632-166368	Sequence 166368,
20	16	88.9	745	15	US-10-027-632-166368	Sequence 166368,
21	16	88.9	774	17	US-10-767-701-14922	Sequence 14922, A
22	16	88.9	1345	10	US-09-943-115A-1	Sequence 1, Appl1
23	16	88.9	1345	14	US-10-146-575-3	Sequence 3, Appl1
24	16	88.9	1345	14	US-10-085-612-3	Sequence 3, Appl1
25	16	88.9	2270	15	US-10-177-917-1	Sequence 1, Appl1
26	16	88.9	3881	10	US-09-948-820-20	Sequence 20, Appl
27	16	88.9	3881	18	US-10-613-076-20	Sequence 20, Appl
28	16	88.9	88493	17	US-10-322-281-703	Sequence 703, App
29	15.4	85.6	19	10	US-09-943-115A-3	Sequence 3, Appl1
30	15.4	85.6	19	14	US-10-146-575-44	Sequence 44, Appl
31	15.4	85.6	299	9	US-09-783-590-3955	Sequence 3955, Ap
32	15.4	85.6	314	18	US-10-437-963-49508	Sequence 49508, A
33	15.4	85.6	314	17	US-10-425-115-40247	Sequence 40247, A
34	15.4	85.6	341	17	US-10-437-963-19690	Sequence 19690, A
35	15.4	85.6	361	16	US-10-424-599-6641	Sequence 6641, Ap
36	15.4	85.6	514	18	US-10-425-115-105065	Sequence 105065,
37	15.4	85.6	591	13	US-10-027-632-286257	Sequence 286257,
38	15.4	85.6	591	13	US-10-027-632-286257	Sequence 286257,
39	15.4	85.6	592	13	US-10-027-632-321713	Sequence 321713,
40	15.4	85.6	592	13	US-10-027-632-321714	Sequence 321714,
41	15.4	85.6	592	15	US-10-027-632-321713	Sequence 321713,
42	15.4	85.6	592	15	US-10-027-632-321713	Sequence 321714,
43	15.4	85.6	599	17	US-10-437-963-10910	Sequence 10910, A
44	15.4	85.6	618	13	US-10-027-632-105305	Sequence 105305,
45	15.4	85.6	618	15	US-10-027-632-105305	Sequence 105305,

ALIGNMENTS

RESULT 1
US-10-085-612-1
Sequence 1, Application US/10085612
Publication No. US20030096251A1
GENERAL INFORMATION:
APPLICANT: Guida, Marco
APPLICANT: Hall, Jeff
APPLICANT: Petros, William
APPLICANT: Vredenburg, James
APPLICANT: Colvin, Oliver
APPLICANT: Marks, Jeffrey
TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
FILE REFERENCE: 4389-5-C1
CURRENT APPLICATION NUMBER: US/10/085,612
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/144,367
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/271,630
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1.
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-612-1
Query Match 100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 18; Conservative 0; Mismatches 0; Gaps 0;
DB 1 GACAAAGGCAGACAGAG 18
1 GACAAAGGCAGACAGAG 18

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RESULT 2
US-10-146-575-13/c
; Sequence 13, Application US/10146575
; Publication No. US20030059800A1
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/10/146,575
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US/09/144,367
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 29
; TYPE: DNA
; ORGANISM: H. sapiens
US-10-146-575-13
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Query Match          91.1%; Score 16.4; DB 14; Length 29;
Best Local Similarity 94.4%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 GACAAGGCGACGACAGAG 18
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Db      24 GACAAGGCGACGACAGAG 7
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RESULT 3
US-10-027-632-106890/c
; Sequence 106890, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106890
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-106890
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Query Match          91.1%; Score 16.4; DB 13; Length 529;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db      170 GTCAGGCGACGACAGAG 153
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RESULT 4
US-10-027-632-106890/c
; Sequence 106890, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106890
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-106890
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Query Match          91.1%; Score 16.4; DB 15; Length 529;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 GACAAGGCGACGACAGAG 18
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Db      170 GTCAGGCGACGACAGAG 153
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RESULT 5
US-10-027-632-25159
; Sequence 25159, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25159
; LENGTH: 714
; TYPE: DNA
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ORGANISM: Human
US-10-027-632-25159

Query Match 91.1%; Score 16.4; DB 13; Length 714;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GACAGGGCAGACAGAG 18
DB 361 GTCAGGGCAGACAGAG 378

RESULT 6
US-10-027-632-25159

Sequence 25159, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

PRIOR FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 25159

LENGTH: 714

TYPE: DNA

ORGANISM: Human

US-10-027-632-25159

Query Match 91.1%; Score 16.4; DB 15; Length 714;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GACAGGGCAGACAGAG 18
DB 361 GTCAGGGCAGACAGAG 378

RESULT 7
US-10-198-846-10434

Sequence 10434, Application US/10198846

Publication No. US2003009974A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Xu, Yongyao

APPLICANT: Wang, Youzhen

APPLICANT: Steinhmann, Kathleen

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS

FILE REFERENCE: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

FILE REFERENCE: MRI-049

CURRENT APPLICATION NUMBER: US/10/198,846

PRIOR FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/306,220

NUMBER OF SEQ ID NOS: 14084

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10434

LENGTH: 1530

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: 897, 1528, 1529, 1530

OTHER INFORMATION: n = A,T,C or G

Query Match 91.1%; Score 16.4; DB 14; Length 1530;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GACAGGGCAGACAGAG 18
DB 997 GACAGGGCAGACAGAG 1014

RESULT 8
US-10-317-277A-4/C

Sequence 4, Application US/10317277A

Publication No. US20040110159A1

GENERAL INFORMATION:

APPLICANT: Dobie, Kenneth W.

TITLE OF INVENTION: Modulation of Estrogen-Responsive Finger Protein Expression

FILE REFERENCE: RPS-0473

CURRENT APPLICATION NUMBER: US/10/317,277A

PRIOR FILING DATE: 2002-12-10

NUMBER OF SEQ ID NOS: 168

SOFTWARE: PatentIn version 3.2

SEQ ID NO 4

LENGTH: 24295

TYPE: DNA

ORGANISM: Homo sapiens

US-10-317-277A-4

Query Match 91.1%; Score 16.4; DB 17; Length 24295;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GACAGGGCAGACAGAG 18
DB 20551 GTCAGGGCAGACAGAG 20534

RESULT 9
US-10-087-192-805

Sequence 805, Application US/10087192

Publication No. US20020182586A1

GENERAL INFORMATION:

APPLICANT: Morris, David W.

APPLICANT: Engelhard, Eric K.

TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR

FILE REFERENCE: CANCER

CURRENT APPLICATION NUMBER: US/10/087,192

PRIOR FILING DATE: 2002-03-01

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 09/798,586

PRIOR FILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 2059

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 805

LENGTH: 25543

TYPE: DNA

ORGANISM: Mus musculus

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)..(25543)

OTHER INFORMATION: n = A,T,C or G

US-10-087-192-805

Query Match 91.1%; Score 16.4; DB 13; Length 25543;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GACAAAGGCGACGACGAG 18
|||||
Db 6541 GACAAAGGCGACGACGAG 6558

RESULT 10
US-10-087-192-1915
; Sequence 1915, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1915
; LENGTH: 34455
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) .. (34455)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1915

Query Match 91.1%; Score 16.4; DB 13; Length 34455;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GACAAAGGCGACGACGAG 18
|||||
Db 2799 GACAAAGGCGACGACGAG 2816

RESULT 11
US-10-087-192-355/c
; Sequence 355, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 355
; LENGTH: 71251
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) .. (71251)
; OTHER INFORMATION: n = A,T,C or G

US-10-087-192-355

Query Match 91.1%; Score 16.4; DB 13; Length 71251;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GACAAAGGCGACGACGAG 18
|||||
Db 43322 GACAAAGGCGACGACGAG 43305

RESULT 12
US-10-087-192-1636/c
; Sequence 1636, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1636
; LENGTH: 73771
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) .. (73771)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1636

Query Match 91.1%; Score 16.4; DB 13; Length 73771;
Best Local Similarity 94.4%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GACAAAGGCGACGACGAG 18
|||||
Db 66831 GACAAAGGCGACGACGAG 66814

RESULT 13
US-10-270-336-3
; Sequence 3, Application US/10270336
; Publication No. US20030074678A1
; GENERAL INFORMATION:
; APPLICANT: ZHU, ShiaoPing et al.
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: CLO01146CON
; CURRENT APPLICATION NUMBER: US/10/270,336
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/270,873
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 119596
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) .. (119596)
; OTHER INFORMATION: n = A,T,C or G
US-10-270-336-3

Query Match 91.1%; Score 16.4; DB 14; Length 119596;
Best Local Similarity 94.4%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GACAAAGGCGACAGACAG 18
DB 63483 GACAAAGGCGACAGACAG 63500

RESULT 14
US-09-805-458A-3
Sequence 3, Application US/09805458A
Patent No. US20020042100A1
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al
TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS,
FILE REFERENCE: CL000722
CURRENT APPLICATION NUMBER: US/09/805,458A
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 172637
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(172637)
OTHER INFORMATION: n = A,T,C or G
US-09-805-458A-3

Query Match 91.1%; Score 16.4; DB 9; Length 172637;
Best Local Similarity 94.4%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GACAAAGGCGACAGACAG 18
DB 95503 GACAAAGGCGACAGACAG 95520

RESULT 15
US-10-433-580-2
Sequence 2, Application US/10433580
Publication No. US20040091497A1
GENERAL INFORMATION:
APPLICANT: GENSET
TITLE OF INVENTION: SCHIZOPHRENIA RELATED VOLTAGE-GATED ION CHANNEL GENE AND PROTEIN
FILE REFERENCE: 93.WOI
CURRENT APPLICATION NUMBER: US/10/433,580
CURRENT FILING DATE: 2003-06-04
PRIOR APPLICATION NUMBER: US 60/251,317
PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent.pm
SEQ ID NO 2
LENGTH: 237961
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: exon
LOCATION: 43726..43868
OTHER INFORMATION: exon 8
FEATURE:
NAME/KEY: exon
LOCATION: 43998..44102
OTHER INFORMATION: exon 9
FEATURE:
NAME/KEY: exon
LOCATION: 52093..52179
OTHER INFORMATION: exon 10

FEATURE:
NAME/KEY: exon
LOCATION: 77568..77699
OTHER INFORMATION: exon 11
FEATURE:
NAME/KEY: exon
LOCATION: 98226..98393
OTHER INFORMATION: exon 12
FEATURE:
NAME/KEY: exon
LOCATION: 106567..106758
OTHER INFORMATION: exon 13
FEATURE:
NAME/KEY: exon
LOCATION: 144109..144246
OTHER INFORMATION: exon 14
FEATURE:
NAME/KEY: exon
LOCATION: 159794..159868
OTHER INFORMATION: exon 15
FEATURE:
NAME/KEY: exon
LOCATION: 191292..191428
OTHER INFORMATION: exon 16
FEATURE:
NAME/KEY: exon
LOCATION: 192867..193108
OTHER INFORMATION: exon 17
FEATURE:
NAME/KEY: exon
LOCATION: 211540..211613
OTHER INFORMATION: exon 18
FEATURE:
NAME/KEY: exon
LOCATION: 225006..225107
OTHER INFORMATION: exon 19
FEATURE:
NAME/KEY: exon
LOCATION: 225544..225613
OTHER INFORMATION: exon 20
FEATURE:
NAME/KEY: exon
LOCATION: 228450..228541
OTHER INFORMATION: exon 21
FEATURE:
NAME/KEY: exon
LOCATION: 228630..228752
OTHER INFORMATION: exon 22
FEATURE:
NAME/KEY: exon
LOCATION: 231289..231345
OTHER INFORMATION: exon 23
FEATURE:
NAME/KEY: exon
LOCATION: 231589..231709
OTHER INFORMATION: exon 24
FEATURE:
NAME/KEY: exon
LOCATION: 231813..231944
OTHER INFORMATION: exon 25
FEATURE:
NAME/KEY: exon
LOCATION: 232800..233067
OTHER INFORMATION: exon 26
FEATURE:
NAME/KEY: exon
LOCATION: 235355..235459
OTHER INFORMATION: exon 27
FEATURE:
NAME/KEY: allele
LOCATION: 51090
OTHER INFORMATION: 99-79335-60 : polymorphic base C or T
FEATURE:

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? NAME/KEY: allele
? LOCATION: 61293
? OTHER INFORMATION: 99-79336-369 : polymorphic base A or G
? FEATURE:
? NAME/KEY: allele
? LOCATION: 80602
? OTHER INFORMATION: 99-79338-332 : polymorphic base C or T
? FEATURE:
? NAME/KEY: allele
? LOCATION: 100485
? OTHER INFORMATION: 99-79314-201 : polymorphic base G or T
? FEATURE:
? NAME/KEY: allele
? LOCATION: 100509
? OTHER INFORMATION: 99-79314-225 : polymorphic base A or G
? FEATURE:
? NAME/KEY: allele
? LOCATION: 106725
? OTHER INFORMATION: 99-79316-158 : polymorphic base C or T
? FEATURE:
? NAME/KEY: allele
? LOCATION: 166087
? OTHER INFORMATION: 99-79322-224 : polymorphic base G or T
? FEATURE:
? NAME/KEY: allele
? LOCATION: 166336
? OTHER INFORMATION: 99-79322-473 : polymorphic base A or G
? FEATURE:
? NAME/KEY: allele
? LOCATION: 235894
? OTHER INFORMATION: 99-79306-182 : polymorphic base C or T
? FEATURE:
? NAME/KEY: primer_bind
? LOCATION: 51031..51051
? OTHER INFORMATION: 99-79335.pu
? FEATURE:
? NAME/KEY: primer_bind
? LOCATION: 51539..51559
? OTHER INFORMATION: 99-79335.rp complement
? FEATURE:
? NAME/KEY: primer_bind
? LOCATION: 60925..60945
? OTHER INFORMATION: 99-79336.pu
? FEATURE:
? NAME/KEY: primer_bind
? LOCATION: 61354..61374
? OTHER INFORMATION: 99-79336.rp complement
? FEATURE:
? NAME/KEY: primer_bind
? LOCATION: 80271..80290
? OTHER INFORMATION: 99-79338.pu
? FEATURE:
? NAME/KEY: primer_bind
? LOCATION: 80700..80720
? OTHER INFORMATION: 99-79338.rp complement
? FEATURE:
? NAME/KEY: primer_bind
? LOCATION: 91037..91056
? OTHER INFORMATION: 99-79339.pu
? FEATURE:
? NAME/KEY: primer_bind
? LOCATION: 91466..91486
? OTHER INFORMATION: 99-79339.rp complement
? FEATURE:
? NAME/KEY: primer_bind
? LOCATION: 100285..100305
? OTHER INFORMATION: 99-79314.pu
? FEATURE:
? NAME/KEY: primer_bind
? LOCATION: 100764..100784
? OTHER INFORMATION: 99-79314.rp complement
? FEATURE:
? NAME/KEY: primer_bind

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? LOCATION: 106568..106585
? OTHER INFORMATION: 99-79316.pu
? FEATURE:
? NAME/KEY: primer_bind
? LOCATION: 107000..107020
? OTHER INFORMATION: 99-79316.rp complement
? FEATURE:
? NAME/KEY: primer_bind
? LOCATION: 165864..165884
? OTHER INFORMATION: 99-79322.pu
? FEATURE:
? NAME/KEY: primer_bind
? LOCATION: 166381..166401
? OTHER INFORMATION: 99-79322.rp complement
? FEATURE:
? NAME/KEY: primer_bind
? LOCATION: 235713..235732
? OTHER INFORMATION: 99-79306.pu
? FEATURE:
? NAME/KEY: primer_bind
? LOCATION: 236190..236210
? OTHER INFORMATION: 99-79306.rp complement
? FEATURE:
? NAME/KEY: primer_bind
? LOCATION: 51071..51089
? OTHER INFORMATION: 99-79335-60.mis

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Query Match 91.1%; Score 16.4; DB 16; Length 237961;
Best Local Similarity 94.4%; Pred. No. 1e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GACAAAGGCGACGACGAG 18
Db 29559 GACAAAGGCGACGACGAG 29576

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Search completed: January 26, 2005, 18:15:43
 Job time : 129.6 secs

Query Match 67.1%; Score 22.8; DB 3; Length 1345;
Best Local Similarity 92.3%; Pred. No. 6.7;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGCCTACTGCTGCAGCTGCAGCCCCG 34
Db 1035 TGCCTACTGCTGCAGCTGCAGCCCCG 1060

RESULT 3

US-09-144-367-3
; Sequence 3, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0)...(0)
US-09-144-367-3

Query Match 67.1%; Score 22.8; DB 4; Length 1345;
Best Local Similarity 92.3%; Pred. No. 6.7;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGCCTACTGCTGCAGCTGCAGCCCCG 34
Db 1035 TGCCTACTGCTGCAGCTGCAGCCCCG 1060

RESULT 4

US-09-489-039A-2633/C
; Sequence 2633, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 2633
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2633

Query Match 61.2%; Score 20.8; DB 4; Length 1023;
Best Local Similarity 78.1%; Pred. No. 38;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 ATTCTTGTCTACTGCTGCAGCTGCAGCCCCG 34
Db 477 ATTATTTGCTACTGTCTCGGACATCAACCCCG 446

RESULT 5

US-09-270-767-6152
; Sequence 6152, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6152
; LENGTH: 445
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-6152

Query Match 60.6%; Score 20.6; DB 4; Length 445;
Best Local Similarity 85.2%; Pred. No. 40;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 8 TTGCTACTGCTGCAGCTGCAGCCCCG 34
Db 373 TCGCTACGAGCTGCAGCTGCAGCACCG 399

RESULT 6

US-09-270-767-21434
; Sequence 21434, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21434
; LENGTH: 445
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-21434

Query Match 60.6%; Score 20.6; DB 4; Length 445;
Best Local Similarity 85.2%; Pred. No. 40;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 8 TTGCTACTGCTGCAGCTGCAGCCCCG 34
Db 373 TCGCTACGAGCTGCAGCTGCAGCACCG 399

RESULT 7

US-09-394-142B-23/C
; Sequence 23, Application US/09394142B
; Patent No. 6696558
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Takayama, Shinichi
; TITLE OF INVENTION: BAG Proteins and Nucleic Acid Molecules Encoding
; FILE REFERENCE: P-LJ 3737
; CURRENT APPLICATION NUMBER: US/09/394,142B
; CURRENT FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 09/150,489
; PRIOR FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0

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Query Match          58.8%; Score 20; DB 3; Length 357;
Best Local Similarity 82.1%; Pred. No. 65;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0.

QY      6 CTTTGCTACTGCGCTGCAGACCTGCACCCCC 33
        ||| ||| ||| ||| ||| ||| |||
Db       35 CTTGGGCGCTGGCTGCAGCTGCTCCCC 8

RESULT 10
US-09-593-483-1/c
: Sequence 1, Application US/09593483
: Patent No. 6410715
:
: GENERAL INFORMATION:
: APPLICANT: NAHUM SONENBERG
:
: ARNIM PAUSE
:
: JOE B. HARFORD
:
: VINCENT J. MILES
:

```

TITLE OF INVENTION: METHODS FOR TREATING
HORMONE DISORDERS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/593,483
FILING DATE: 14-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/294,143
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/060
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-593-483-1

Query Match 58.8%; Score 20; DB 4; Length 357;
Best Local Similarity 82.1%; Pred. No. 65;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 6 CTTTGCTACTGGCTGCAGCTGCAGCCCC 33
Db 35 CTTGGGCTGCTGCTGCAGCTGCTGCCCC 8

RESULT 11
US-09-023-655-1445/c
Sequence 1445, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1445:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9561629
US-09-023-655-1445

Query Match 58.8%; Score 20; DB 4; Length 357;
Best Local Similarity 82.1%; Pred. No. 65;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 6 CTTTGCTACTGGCTGCAGCTGCAGCCCC 33
Db 35 CTTGGGCTGCTGCTGCAGCTGCTGCCCC 8

RESULT 12
US-08-294-143-3/c
Sequence 3, Application US/08294143
Patent No. 5874231
GENERAL INFORMATION:
APPLICANT: NAHUM SONENBERG
APPLICANT: ARNIM PAUSE
APPLICANT: JOE B. HARFORD
APPLICANT: VINCENT J. MILES
TITLE OF INVENTION: METHODS FOR TREATING
TITLE OF INVENTION: HORMONE DISORDERS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,143
FILING DATE: August 22, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/060
TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 829 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-294-143-3

Query Match 58.8%; Score 20; DB 2; Length 829;
Best Local Similarity 82.1%; Pred. No. 76;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 CTTTGCTACTGCTGCAGCTGCAGCCCC 33
DB 62 CTTGGGGCTGTGGCTGCAGCTGTGCCCC 35

RESULT 13

US-09-256-331-3/C
Sequence 3, Application US/09256331
Patent No. 611077
GENERAL INFORMATION:
APPLICANT: NAHUM SONENBERG
APPLICANT: ARNIM PAUSE
APPLICANT: JOE B. HARFORD
TITLE OF INVENTION: METHODS FOR TREATING
TITLE OF INVENTION: HORMONE DISORDERS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/256,331
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/294,143
FILING DATE: August 22, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/060
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 829 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-256-331-3

Query Match 58.8%; Score 20; DB 3; Length 829;
Best Local Similarity 82.1%; Pred. No. 76;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 CTTTGCTACTGCTGCAGCTGCAGCCCC 33
DB 62 CTTGGGGCTGTGGCTGCAGCTGTGCCCC 35

RESULT 14
US-09-593-483-3/C
Sequence 3, Application US/09593483
Patent No. 6410715
GENERAL INFORMATION:
APPLICANT: NAHUM SONENBERG
APPLICANT: ARNIM PAUSE
APPLICANT: JOE B. HARFORD
TITLE OF INVENTION: METHODS FOR TREATING
TITLE OF INVENTION: HORMONE DISORDERS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/593,483
FILING DATE: 14-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/294,143
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/060
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 829 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-593-483-3

Query Match 58.8%; Score 20; DB 4; Length 829;
Best Local Similarity 82.1%; Pred. No. 76;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 CTTTGCTACTGCTGCAGCTGCAGCCCC 33
DB 62 CTTGGGGCTGTGGCTGCAGCTGTGCCCC 35

RESULT 15
US-09-489-039A-5244/C
Sequence 5244, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 13:15:32 ; Search time 241.022 Seconds
(without alignments)
810.549 Million cell updates/sec

Title: US-10-085-612A-2

Perfect score: 34
Sequence: 1 cgaattcttctactgctgcagctgcagcccg 34

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09C_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10E_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	34	US-10-085-612-2	Sequence 2, Appl1
2	33	97.1	34	US-10-085-612-6	Sequence 6, Appl1
3	33	97.1	1254	US-10-085-612-4	Sequence 4, Appl1
4	22.8	67.1	1012	US-09-957-997-4	Sequence 1, Appl1
5	22.8	67.1	1345	US-09-943-115A-1	Sequence 3, Appl1
6	22.8	67.1	1345	US-10-146-575-3	Sequence 3, Appl1
7	22.8	67.1	1345	US-10-085-612-3	Sequence 1, Appl1
8	22.8	67.1	11186	US-09-957-997-1	Sequence 1, Appl1
9	22.8	67.1	13035	US-10-121-960C-14	Sequence 14, Appl1
10	22.8	67.1	15185	US-10-121-960C-17	Sequence 17, Appl1
11	21.6	63.5	481	US-10-027-632-72580	Sequence 72580, A
12	21.6	63.5	481	US-10-027-632-72580	Sequence 72580, A

C	13	21.4	62.9	599	13	US-10-027-632-285947	Sequence 285947,
C	14	21.4	62.9	599	15	US-10-027-632-285947	Sequence 285947,
C	15	21.4	62.9	3800	16	US-10-240-425-355	Sequence 355, App
C	16	21.4	61.8	1442	16	US-10-424-599-64169	Sequence 64169, A
C	17	20.8	61.2	976	16	US-10-282-122A-23816	Sequence 23816, A
C	18	20.6	60.6	30	15	US-10-215-432-41	Sequence 41, Appl1
C	19	20.2	59.4	394	16	US-10-424-599-31369	Sequence 31369, A
C	20	20.2	59.4	470	10	US-09-918-995-24594	Sequence 24594, A
C	21	20.2	59.4	672	13	US-10-027-632-253693	Sequence 253693,
C	22	20.2	59.4	672	13	US-10-027-632-253693	Sequence 253693,
C	23	20.2	59.4	923	16	US-10-425-114-34526	Sequence 34526, A
C	24	20.2	59.4	968	18	US-10-739-930-2556	Sequence 2556, Ap
C	25	20.2	59.4	994	10	US-09-934-455-489	Sequence 489, App
C	26	20.2	59.4	994	17	US-10-767-701-9995	Sequence 9995, Ap
C	27	20.2	59.4	1149	18	US-10-425-115-97578	Sequence 97578, A
C	28	20.2	59.4	4285	17	US-10-303-327-4	Sequence 4, Appl1
C	29	20.2	59.4	4308	10	US-09-394-1428-23	Sequence 23, Appl1
C	30	20.2	59.4	4308	17	US-10-782-627-23	Sequence 23, Appl1
C	31	20.2	59.4	5526	18	US-10-357-930-23191	Sequence 23191, A
C	32	20.2	59.4	5526	18	US-10-357-930-29057	Sequence 29057, A
C	33	20.2	59.4	35425	17	US-10-322-696-91	Sequence 91, Appl1
C	34	20.2	58.8	357	16	US-10-641-643-145	Sequence 145, App
C	35	20.2	58.8	551	18	US-10-723-860-549	Sequence 549, App
C	36	20.2	58.8	627	9	US-09-770-149-726	Sequence 726, App
C	37	20.2	58.8	802	9	US-09-925-301-322	Sequence 322, App
C	38	20.2	58.8	831	15	US-10-353-929-57	Sequence 57, Appl1
C	39	20.2	58.8	1358	10	US-09-877-843-11	Sequence 11, Appl1
C	40	20.2	58.8	1358	16	US-10-403-161-25	Sequence 25, Appl1
C	41	20.2	58.8	2059	16	US-10-276-774-864	Sequence 864, App
C	42	20.2	58.8	2173	16	US-10-425-114-21375	Sequence 21375, A
C	43	20.2	58.8	2758	18	US-10-425-115-3898	Sequence 3898, Ap
C	44	20.2	58.8	13358	18	US-10-719-993-6923	Sequence 6923, Ap
C	45	20.2	58.8	37443	18	US-10-719-993-6853	Sequence 6853, Ap

ALIGNMENTS

RESULT 1
US-10-085-612-2
Sequence 2, Application US/10085612
Publication No. US20030096251A1
GENERAL INFORMATION:
APPLICANT: Guida, Marco
APPLICANT: Hall, Jeff
APPLICANT: Petros, William
APPLICANT: Vredenburg, James
APPLICANT: Colvin, Oliver
APPLICANT: Marks, Jeffrey
TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
FILE REFERENCE: 4389-5-C1
CURRENT APPLICATION NUMBER: US/10/085,612
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/144,367
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/271,630
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 34
TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-612-2
Query Match 100.0%; Score 34; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 34; Conservative 0; Mismatches 0; Gaps 0;
Db 1 CGAATCTTCTACTGCTGCAGCTGCAGCCCG 34
1 CGAATCTTCTACTGCTGCAGCTGCAGCCCG 34

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RESULT 2
US-10-085-612-6
; Sequence 6, Application US/10085612
; Publication No. US20030096251A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Vredenburg, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Marks, Jeffrey
; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
; FILE REFERENCE: 4389-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-612-6

Query Match          97.1%; Score 33; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGATTCCTTGCTACTGGCTGCAGCTGCAGCCCC 33
Db 1 CGATTCCTTGCTACTGGCTGCAGCTGCAGCCCC 33

RESULT 3
US-10-085-612-4
; Sequence 4, Application US/10085612
; Publication No. US20030096251A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Vredenburg, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Marks, Jeffrey
; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
; FILE REFERENCE: 4389-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1254
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-612-4

Query Match          97.1%; Score 33; DB 14; Length 1254;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGATTCCTTGCTACTGGCTGCAGCTGCAGCCCC 33
Db 1 CGATTCCTTGCTACTGGCTGCAGCTGCAGCCCC 33
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Db 1004 CGATTCCTTGCTACTGGCTGCAGCTGCAGCCCC 1036

RESULT 4
US-09-957-997-4
; Sequence 4, Application US/09957997
; Patent No. US20020150915A1
; GENERAL INFORMATION:
; APPLICANT: Berkenstam, Anders
; APPLICANT: Bertilsson, Gran
; APPLICANT: Blomquist, Patrik
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-046001
; CURRENT APPLICATION NUMBER: US/09/957,997
; CURRENT FILING DATE: 2001-09-21
; EARLIER APPLICATION NUMBER: SE 0003393-6
; EARLIER FILING DATE: 2000-09-22
; EARLIER APPLICATION NUMBER: 60/238,895
; EARLIER FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1012
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-957-997-4

Query Match          67.1%; Score 22.8; DB 9; Length 1012;
Best Local Similarity 92.3%; Pred. No. 18;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 9 TGCTACTGGCTGCAGCTGCAGCCCCG 34
Db 947 TGCTACTGGCTGCAGCTGCAGCCCCG 972

RESULT 5
US-09-943-115A-1
; Sequence 1, Application US/09943115A
; Publication No. US20030017469A1
; GENERAL INFORMATION:
; APPLICANT: SEQUENOM, Inc.
; APPLICANT: Risinger, Carl
; APPLICANT: Andersson, Maria
; APPLICANT: Lewander, Tommy
; APPLICANT: Olaisson, Erik
; TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9
; FILE REFERENCE: 52459-20021.00
; CURRENT APPLICATION NUMBER: US/09/943,115A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: UK 0021286.0
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-943-115A-1

Query Match          67.1%; Score 22.8; DB 10; Length 1345;
Best Local Similarity 92.3%; Pred. No. 18;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 9 TGCTACTGGCTGCAGCTGCAGCCCCG 34
Db 1035 TGCTACTGGCTGCAGCTGCAGCCCCG 1060

RESULT 6
US-10-146-575-3
; Sequence 3, Application US/10146575
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: Publication NO. US20030059800A1
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: GENERAL INFORMATION:
:
: APPLICANT: Lichteer, Jay
:
: APPLICANT: Guido, Marco
:
: TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
:
: FILE REFERENCE: SEQ-12P
:
: CURRENT APPLICATION NUMBER: US/10/146,575
:
: PRIOR FILING DATE: 2002-05-14
:
: PRIOR APPLICATION NUMBER: US/09/144,367
:
: PRIOR FILING DATE: 1998-08-31
:
: NUMBER OF SEQ ID NOS: 58
:
: SOFTWARE: FaSTSeq for Windows Version 3.0
:
: SEQ ID NO 3
:
: LENGTH: 1345
:
: TYPE: DNA
:
: ORGANISM: H. sapiens
:
: FEATURE:
:
: NAME/KEY: Other
:
: LOCATION: (0)...(0)
:
: US-10-146-575-3

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Query Match	67.1%	Score 22.8	DB 14	Length 1345
Best Local Similarity	92.3%	Pred. No. 18		
Matches 24	Conservative 0	Mismatches 2	Indels 0	Gaps 0

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Db     1035 TGCTACTGGCTGCAGCTCCAGCCCTG 1060
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RESULT 7
US-10-085-612-3
; Sequence 3, Application US/10085612
; Publication No. US20030096251A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Vredenburg, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Marks, Jeffrey
; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
; TITLE OF INVENTION: Compositions Therefor
; FILE REFERENCE: 4369-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-085-612-3

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Query Match	67.1%	Score 22.8	DB 14	Length 1345
Best Local Similarity	92.3%	Pred. No. 18		
Matches 24	Conservative 0	Mismatches 2	Indels 0	Gaps 0

Oy 9 TGCTACTGGCTGCAGCTGCAGCCCCG 34
Db 1035 TGCTACTGGCTGCAGCTCCAGCCCTG 1060

RESULT 8
US-09-957-997-1
; Sequence 1, Application US/09957997
; Patent No. US20020150915A1
; GENERAL INFORMATION:
; APPLICANT: Berkenstam, Anders

```

1  APPLICANT: Bertilsson, Grah
2  APPLICANT: Blomquist, Patrik
3  TITLE OF INVENTION: PROMOTER SEQUENCES
4  FILE REFERENCE: 13425-046001
5  CURRENT APPLICATION NUMBER: US/09/957, 997
6  CURRENT FILING DATE: 2001-09-21
7  EARLIER APPLICATION NUMBER: SE 0003393-6
8  EARLIER FILING DATE: 2000-09-22
9  EARLIER APPLICATION NUMBER: 60/228, 895
10 EARLIER FILING DATE: 2000-10-10
11 NUMBER OF SEQ ID NOS: 15
12 SOFTWARE: FastSeq for Windows Version 4.0
13 SEQ ID NO 1
14 LENGTH: 11186
15 TYPE: DNA
16 ORGANISM: Homo sapiens
17 US-09-957-997-1

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Query Match	67.1%	Score 22.8	DB 9	Length 1186
Best Local Similarity	92.3%	Pred. No. 21		
Matches 24	Conservative 0	Mismatches 2	Indels 0	Gaps 0

[illegible]

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RESULT 9
US-10-121-960C-14
Sequence 14, Application US/10121960C
Publication No. US20030145341A1
GENERAL INFORMATION:
APPLICANT: ZHANG, Weisheng
APPLICANT: CONTAG, Pamela
APPLICANT: PURCHIO, Anthony
APPLICANT: HASHIMA, Sandy
APPLICANT: MA, Shiley
APPLICANT: NAWOTKA, Kevin
TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
TITLE OF INVENTION: TRANSCRIPTOM CONTROL ELEMENTS ASSOCIATED WITH
TITLE OF INVENTION: CYTOCHROME EXPRESSION
FILE REFERENCE: 9400-0014 / PXE-014-US
CURRENT APPLICATION NUMBER: US/10/121,960C
CURRENT FILING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 13035
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: human CYP3A4 gene locus
US-10-121-960C-14

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Query Match	67.1%	Score 22.8	DB 15	Length 13035
Best Local Similarity	92.3%	Pred. No. 21		
Matches 24; Conservative	0	Mismatches 2	Indels 0	Gaps 0

QY 9 TGTACTGGCTGCAGCTGCAGCCCCG 34
DB 12860 TGTACTGGCTGCAGCTGCAGCCCCG 12885

RESULT 10
US-10-121-960C-17
: Sequence 17, Application US/10121960C
: Publication No. US20030145341A1
: GENERAL INFORMATION:
: APPLICANT: ZHANG, Weisheng
: APPLICANT: CONTAG, Pamela
: APPLICANT: PURCHIO, Anthony
: APPLICANT: HASHIMA, Sandy
: APPLICANT: MA, Shitley

```

; APPLICANT: NAMOTKA, Kevin
; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
; TITLE OF INVENTION: TRANSCRIPTION CONTROL ELEMENTS ASSOCIATED WITH
; TITLE OF INVENTION: CYTOCHROME EXPRESSION
; FILE REFERENCE: 9400-0014 / PEX-014.US
; CURRENT APPLICATION NUMBER: US/10/121,960C
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 15185
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CYP3A4-luc transgene
US-10-121-960C-17

Query Match          67.1%; Score 22.8; DB 15; Length 15185;
Best Local Similarity 92.3%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 9 TGGTACTGCTGCAGTCGACGCCCG 34
Db 12860 TGGTACTGCTGCAGTCGACGCCCTG 12885

RESULT 11
US-10-027-632-72580
; Sequence 72580, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72580
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-72580

Query Match          63.5%; Score 21.6; DB 13; Length 481;
Best Local Similarity 85.7%; Pred. No. 53;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 6 CTTTGCTACTGCTGCAGTCGACGCCCG 33
Db 190 CTATGCTCTGCTGCAGTCGACACACC 217

RESULT 12
US-10-027-632-72580
; Sequence 72580, Application US/10027632
; Publication No. US20020204075A9
; GENERAL INFORMATION:
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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 285947
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-285947

Query Match          62.9%; Score 21.4; DB 13; Length 599;
Best Local Similarity 80.6%; Pred. No. 65;
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Cy 6 CTTTGCTACTGCTGCAGTCGACGCCCG 33
Db 190 CTATGCTCTGCTGCAGTCGACACACC 217

RESULT 13
US-10-027-632-285947/c
; Sequence 285947, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 285947
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-285947
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Qy 3 ATTCTTGTACTGCTGCTGACGCTGACGCCC 33
DB 48 ATTCTTACACCTCTCTGCTGACGCTGACGACC 18

RESULT 14
US-10-027-632-285947/c
; Sequence 285947, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 285947
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-285947

Query Match 62.9%; Score 21.4; DB 15; Length 599;
Best Local Similarity 80.6%; Pred. No. 65;
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 ATTCTTGTACTGCTGCTGACGCTGACGCCC 33
DB 48 ATTCTTACACCTCTCTGCTGACGCTGACGACC 18

RESULT 15
US-10-240-425-355
; Sequence 355, Application US/10240425
; Publication No. US20040033502A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Schert, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 355
; LENGTH: 3800
; TYPE: DNA

; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040033502A1 AB020697
US-10-240-425-355

Query Match 62.9%; Score 21.4; DB 16; Length 3800;
Best Local Similarity 80.6%; Pred. No. 73;
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CGATCTTGTACTGCTGCTGACGCTGACGCC 31
DB 464 CGATCTGACGGCGGCTGACGCTGACGCC 494

Search completed: January 26, 2005, 18:15:45
Job time : 243.022 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 11:30:01 / Search time 30.0667 Seconds
(without alignments)
520.089 Million cell updates/sec

Title: US-10-085-612a-17
Perfect score: 22
Sequence: 1 atctgtagtgctgctgtcg 22

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapept 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA: *
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2: /cgn2_6/pdata/1/ina/5B.COMB.seq: *
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5: /cgn2_6/pdata/1/ina/PCTUS.COMB.seq: *
6: /cgn2_6/pdata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	1345	US-09-372-339-1	Sequence 1, Appl
2	22	100.0	1345	US-09-372-339-2	Sequence 2, Appl
3	22	100.0	1345	US-09-144-367-3	Sequence 3, Appl
4	18.8	85.5	5400	US-09-134-000C-1773	Sequence 1773, Ap
5	17.2	78.2	752	US-09-008-979A-8	Sequence 8, Appl
6	17.2	78.2	752	US-09-460-618-8	Sequence 8, Appl
7	17.2	78.2	752	US-09-310-235B-8	Sequence 8, Appl
8	16.2	73.6	211	US-09-513-999C-21256	Sequence 21256, A
9	16.2	73.6	428	US-09-621-976-15687	Sequence 15687, A
10	16.2	73.6	640	US-09-034-088A-26	Sequence 26, Appl
11	16.2	73.6	640	US-09-781-811-26	Sequence 26, Appl
12	16.2	73.6	692	US-08-465-283A-1	Sequence 1, Appl
13	16.2	73.6	692	US-08-463-387A-1	Sequence 1, Appl
14	16.2	73.6	692	US-09-102-977-1	Sequence 1, Appl
15	16.2	73.6	692	US-09-034-088A-1	Sequence 1, Appl
16	16.2	73.6	692	US-09-781-811-1	Sequence 1, Appl
17	15.8	71.8	96109	US-09-596-002-35	Sequence 35, Appl
18	15.8	71.8	99916	US-09-816-095-3	Sequence 3, Appl
19	15.6	70.9	343	US-09-621-976-654	Sequence 654, App
20	15.6	70.9	393	US-09-270-767-7434	Sequence 27434, A
21	15.6	70.9	441	US-09-248-796A-11615	Sequence 11615, A
22	15.6	70.9	834	US-09-543-681A-355	Sequence 355, App
23	15.6	70.9	975	US-09-543-681A-3164	Sequence 3164, App
24	15.6	70.9	1353	US-09-270-767-11795	Sequence 11795, A
25	15.6	70.9	1379	US-09-437-607A-1	Sequence 1, Appl
26	15.6	70.9	1380	US-08-437-607A-4	Sequence 4, Appl
27	15.6	70.9	2733	US-08-676-967-3	Sequence 3, Appl

C	28	15.6	70.9	2733	1	US-08-676-974-3	Sequence 3, Appl
C	29	15.6	70.9	2733	2	US-09-098-487-3	Sequence 3, Appl
C	30	15.6	70.9	75395	4	US-09-984-890-3	Sequence 3, Appl
C	31	15.6	70.9	75395	4	US-10-274-194-3	Sequence 3, Appl
C	32	15.4	70.0	11212	4	US-09-248-796A-2520	Sequence 2520, Ap
C	33	15.4	70.0	1650	4	US-09-579-288-3	Sequence 3, Appl
C	34	15.4	70.0	2403	4	US-09-907-794A-226	Sequence 226, App
C	35	15.4	70.0	2403	4	US-09-905-125A-226	Sequence 226, App
C	36	15.4	70.0	2403	4	US-09-902-775A-226	Sequence 226, App
C	37	15.4	70.0	2403	4	US-09-906-700-226	Sequence 226, App
C	38	15.4	70.0	2403	4	US-09-903-603A-226	Sequence 226, App
C	39	15.4	70.0	2534	4	US-09-579-288-1	Sequence 1, Appl
C	40	15.4	70.0	2534	4	US-09-579-288-4	Sequence 1, Appl
C	41	15.2	69.1	443	4	US-09-513-999C-31715	Sequence 31715, A
C	42	15.2	69.1	450	4	US-09-540-236-681	Sequence 681, App
C	43	15.2	69.1	488	4	US-09-621-976-2091	Sequence 2091, App
C	44	15.2	69.1	493	4	US-09-621-976-16615	Sequence 16615, A
C	45	15.2	69.1	544	4	US-09-513-999C-12485	Sequence 12485, A

ALIGNMENTS

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RESULT 1
US-09-372-339-1
Sequence 1, Application US/09372339
Patent No. 6174684
GENERAL INFORMATION:
APPLICANT: Redbeck, Timothy
APPLICANT: Felix, Carolyn
TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
FILE REFERENCE: PENN-0695
CURRENT FILING DATE: 1999-08-11
EARLIER APPLICATION NUMBER: US/09/372,339
EARLIER FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1345
TYPE: DNA
ORGANISM: Homo sapiens
US-09-372-339-1

Query Match      100.0%; Score 22; DB 3; Length 1345;
Best Local Similarity 100.0%; Pred. No. 0.17; Mismatches 0; Gaps 0;
Matches 22; Conservative 0; Indels 0;

Cy      1 ATCTGTAGTGCTGCTGTGG 22
Db      745 ATCTGTAGTGCTGCTGTGG 766

RESULT 2
US-09-372-339-2
Sequence 2, Application US/09372339
Patent No. 6174684
GENERAL INFORMATION:
APPLICANT: Redbeck, Timothy
APPLICANT: Felix, Carolyn
TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
FILE REFERENCE: PENN-0695
CURRENT FILING DATE: 1999-08-11
EARLIER APPLICATION NUMBER: US/09/372,339
EARLIER FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1345
TYPE: DNA
ORGANISM: Homo sapiens
US-09-372-339-2
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Query Match 100.0%; Score 22; DB 3; Length 1345;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCTGTAGTGTGCTTGTGG 22
|||||
Db 745 ATCTGTAGTGTGCTTGTGG 766

RESULT 3
US-09-144-367-3
; Sequence 3, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0)...(0)
US-09-144-367-3

Query Match 100.0%; Score 22; DB 4; Length 1345;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCTGTAGTGTGCTTGTGG 22
|||||
Db 745 ATCTGTAGTGTGCTTGTGG 766

RESULT 4
US-09-134-000C-1773/C
; Sequence 1773, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1773
; LENGTH: 5400
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (30)...(30)
; OTHER INFORMATION: Nucleotide 30 is "n" wherein "n" = any nucleotide.
US-09-134-000C-1773

Query Match 85.5%; Score 18.8; DB 4; Length 5400;
Best Local Similarity 90.9%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATCTGTAGTGTGCTTGTGG 22

Db 3834 ATCTGAAGTGTGCTTGTGG 3813
|||||

RESULT 5
US-09-008-979A-8
; Sequence 8, Application US/0908979A
; Patent No. 6080914
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; TITLE OF INVENTION: Strawberry Promoters and Genes
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carmen Rodriguez, Paralegal, Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,979A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Kammerer, Patricia A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: MOBT:058 (38-21(10613)A)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1438
; TELEFAX: (713) 789-2679
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-008-979A-8

Query Match 78.2%; Score 17.2; DB 3; Length 752;
Best Local Similarity 86.4%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATCTGTAGTGTGCTTGTGG 22
|||||
Db 305 ATCTGTAGTGTGCTTGTGG 326

RESULT 6
US-09-460-618-8
; Sequence 8, Application US/09460618
; Patent No. 6235482
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; TITLE OF INVENTION: Strawberry Promoters and Genes
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carmen Rodriguez, Paralegal, Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/460,618
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/008,979
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT-058 (38-21(10613)A)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1438
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-460-618-6

Query Match 78.2%; Score 17.2; DB 3; Length 752;
Best Local Similarity 86.4%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATCTGTAGTGTGGCTTGTGG 22
DB 305 ATCTGTAGTGTACCTTGTGG 326

RESULT 7
US-09-310-2358-8
Sequence 8, Application US/093102358
Patent No. 6392030
GENERAL INFORMATION:
APPLICANT: Comer, Timothy
TITLE OF INVENTION: STRAMBERY PROMOTERS AND GENES
FILE REFERENCE: MOBT058-1 (11899,0058, DVUS00)
CURRENT APPLICATION NUMBER: US/09/310,2358
CURRENT FILING DATE: 1998-05-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 752
TYPE: DNA
ORGANISM: fragaria x ananassa
US-09-310-2358-8

Query Match 78.2%; Score 17.2; DB 3; Length 752;
Best Local Similarity 86.4%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATCTGTAGTGTGGCTTGTGG 22
DB 305 ATCTGTAGTGTACCTTGTGG 326

RESULT 8
US-09-513-999C-21256/c
Sequence 21256, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm
SEQ ID NO 21256
LENGTH: 211;
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 13
OTHER INFORMATION: r=a or g
US-09-513-999C-21256

Query Match 73.6%; Score 16.2; DB 4; Length 211;
Best Local Similarity 85.7%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATCTGTAGTGTGGCTTGTGG 21
DB 195 ATCTGTAGTGTGGCTTGTGG 175

RESULT 9
US-09-621-976-15687
Sequence 15687, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET, 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 15687
LENGTH: 428
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-15687

Query Match 73.6%; Score 16.2; DB 4; Length 428;
Best Local Similarity 85.7%; Pred. No. 86;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATCTGTAGTGTGGCTTGTGG 21
DB 329 ATCTGTAGTGTGGCTTGTGG 349

RESULT 10
US-09-034-088A-26
Sequence 26, Application US/09034088A
Patent No. 6310034
GENERAL INFORMATION:
APPLICANT: WOYCHIK, RICHARD P.
APPLICANT: BULTMAN, SCOTT J.
APPLICANT: MITCHARD, EDWARD J.
TITLE OF INVENTION: METHODS AND POLYPEPTIDES ENCODED BY AGOUTI GENE
FILE REFERENCE: 4310,001600
CURRENT APPLICATION NUMBER: US/09/034,088A
CURRENT FILING DATE: 1998-03-03
PRIOR APPLICATION NUMBER: 08/064,385
PRIOR FILING DATE: 1993-05-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 640
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-034-088A-26

Query Match 73.6%; Score 16.2; DB 3; Length 640;
Best Local Similarity 85.7%; Pred. No. 92;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCTGTAGTGTGGCTTGTGG 22
Db 515 TCTGTGGTGGGCTTGTGG 535

RESULT 11

US-09-781-811-26
Sequence 26, Application US/09781811
Patent No. 6514747
GENERAL INFORMATION:
APPLICANT: WOYCHIK, RICHARD P.
APPLICANT: BULTMAN, SCOTT J.
APPLICANT: MICHAUD, EDWARD J.
TITLE OF INVENTION: AGOUTI POLYNUCLEOTIDE COMPOSITIONS AND METHODS OF USE
FILE REFERENCE: 4310.001682
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 09/034,088
PRIOR FILING DATE: 1998-03-03
PRIOR APPLICATION NUMBER: 08/064,385
PRIOR FILING DATE: 1993-05-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 640
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-781-811-26

Query Match 73.6%; Score 16.2; DB 4; Length 640;
Best Local Similarity 85.7%; Pred. No. 92;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCTGTAGTGTGGCTTGTGG 22
Db 515 TCTGTGGTGGGCTTGTGG 535

RESULT 12

US-08-465-293A-1
Sequence 1, Application US/08465293A
Patent No. 5789651
GENERAL INFORMATION:
APPLICANT: WOYCHIK, RICHARD P.
TITLE OF INVENTION: Isolation and Characterization of
TITLE OF INVENTION: Agouti A Diabetes/Obesity Related Gene.
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
STREET: 555 13th Street, N.W., Suite #480 West
CITY: Washington
STATE: District of Columbia
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,293A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,385
FILING DATE: 21-MAY-1993

ATTORNEY/AGENT INFORMATION:
NAME: Edward A. Pennington
REGISTRATION NUMBER: 32,588
REFERENCE/DOCKET NUMBER: 2240-7054
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 857-7887
TELEFAX: (202) 857-7929
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 692 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mouse
STRAIN: C3H Strain
DEVELOPMENTAL STAGE: Neonatal or Adult
TISSUE TYPE: Neonatal skin or adult Ay 129/Sv kidney or
TISSUE TYPE: testis.
IMMEDIATE SOURCE:
LIBRARY: Neonatal skin cDNA
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Agouti locus of mouse chromosome 2.
FEATURE:
NAME/KEY: Agouti locus
IDENTIFICATION METHOD: Experimental
OTHER INFORMATION: In addition to hair color in mice, the
OTHER INFORMATION: Agouti gene is responsible for embryonic lethality, obesity,
OTHER INFORMATION: diabetes, and the development of tumor in a wide variety of
OTHER INFORMATION: tissues.
PUBLICATION INFORMATION:
AUTHORS: Scott J. Boltman, Edward J. Michaud, and Richard
AUTHORS: P. Woychik
TITLE: Molecular Characterization of the Mouse Agouti
TITLE: Locus
JOURNAL: Submitted to CELL
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 692
US-08-465-293A-1

Query Match 73.6%; Score 16.2; DB 1; Length 692;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCTGTAGTGTGGCTTGTGG 22
Db 567 TCTGTGGTGGGCTTGTGG 587

RESULT 13

US-08-463-387A-1
Sequence 1, Application US/08463387A
Patent No. 5843652
GENERAL INFORMATION:
APPLICANT: WOYCHIK, RICHARD P.
TITLE OF INVENTION: Isolation and Characterization of
TITLE OF INVENTION: Agouti A Diabetes/Obesity Related Gene.
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
STREET: 555 13th Street, N.W., Suite #480 West
CITY: Washington
STATE: District of Columbia
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,387A

FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,385
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Edward A. Pennington
REGISTRATION NUMBER: 32,588
REFERENCE/DOCKET NUMBER: 2240-7054
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 857-7887
TELEFAX: (202) 857-7929
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 692 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mouse
STRAIN: C3H Strain
DEVELOPMENTAL STAGE: Neonatal or Adult
TISSUE TYPE: Neonatal skin or adult Ay isigo kidney or
TISSUE TYPE: testis.
IMMEDIATE SOURCE:
LIBRARY: Neonatal skin cDNA
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Agouti locus of mouse chromosome 2.
FEATURE:
NAME/KEY: Agouti locus
IDENTIFICATION METHOD: Experimental
OTHER INFORMATION: In addition to hair color in mice, the
OTHER INFORMATION: Agouti gene is responsible for embryonic lethality, obesity,
OTHER INFORMATION: diabetes, and the development of tumor in a wide variety of
OTHER INFORMATION: tissues.
PUBLICATION INFORMATION:
AUTHORS: Scott J. Boltman, Edward J. Micaud, and Richard
AUTHORS: P. Moychik
TITLE: Molecular Characterization of the Mouse Agouti
TITLE: Locus
JOURNAL: Submitted to CELL
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 692
US-08-463-387A-1
Query Match 73.6%; Score 16.2; DB 2; Length 692;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 2 TCTGTAGTGTGGCTTGTGG 22
DB 567 TCTGTGGTGGGCTTGTGG 587
RESULT 14
US-09-102-977-1
Sequence 1, Application US/09102977
Patent No. 6080550
GENERAL INFORMATION:
APPLICANT: Moychik, Richard P.
TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF AGOUTI
TITLE OF INVENTION: A DIABETES/OBESITY RELATED GENE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,977
FILING DATE: 22-JUN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/899,134
FILING DATE: 23-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/462,732
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ORNL:014--1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512)418-3000
TELEFAX: (512)474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 692 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 83..475
US-09-102-977-1

Query Match 73.6%; Score 16.2; DB 3; Length 692;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 2 TCTGTAGTGTGGCTTGTGG 22
DB 567 TCTGTGGTGGGCTTGTGG 587

RESULT 15
US-09-034-088A-1
Sequence 1, Application US/09034088A
Patent No. 6310034
GENERAL INFORMATION:
APPLICANT: MOYCHIK, RICHARD P.
APPLICANT: BULTMAN, SCOTT J.
APPLICANT: MICHAUD, EDWARD J.
TITLE OF INVENTION: METHODS AND POLYPEPTIDES ENCODED BY AGOUTI GENE
FILE REFERENCE: 4310.001600
CURRENT APPLICATION NUMBER: US/09/034,088A
CURRENT FILING DATE: 1998-03-03
PRIOR APPLICATION NUMBER: 08/064,385
PRIOR FILING DATE: 1993-05-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 692
TYPE: DNA
ORGANISM: Mus musculus
US-09-034-088A-1

Query Match 73.6%; Score 16.2; DB 3; Length 692;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 2 TCTGTAGTGTGGCTTGTGG 22
DB 567 TCTGTGGTGGGCTTGTGG 587

Search completed: January 26, 2005, 13:15:20

Job time : 30.1917 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 13:15:32 ; Search time 155.956 Seconds
(without alignments)
810.549 Million cell updates/sec

Title: US-10-085-612A-17

Perfect score: 22
Sequence: 1 atctgtagctgtgctgtctgtcg 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	1345	10	US-09-943-115A-1
2	22	100.0	1345	14	US-10-146-575-3
3	22	100.0	1345	14	US-10-085-612-3
4	22	100.0	13035	15	US-10-121-960C-14
5	22	100.0	15185	15	US-10-121-960C-17
6	20	90.9	26	18	US-10-114-908-9
7	19.4	88.2	33488	15	US-10-085-117-235
8	18.8	85.5	1012	9	US-09-957-997-4
9	18.8	85.5	7053	9	US-09-070-927A-78
10	18.8	85.5	11186	9	US-09-957-997-1
11	17.8	80.9	1378	9	US-09-820-893-28
12	17.8	80.9	1378	16	US-10-607-565-28

13	17.2	78.2	615	18	US-10-425-115-172581	Sequence 172581,
14	17.2	78.2	1254	14	US-10-085-612-4	Sequence 4, Appl1
15	17.2	78.2	4170	17	US-10-602-441-5	Sequence 5, Appl1
16	17.2	78.2	8943	16	US-10-257-166-47	Sequence 47, Appl1
17	17.2	78.2	130427	14	US-10-175-523-87	Sequence 87, Appl1
18	16.8	76.4	417	17	US-10-437-963-94546	Sequence 94546, A
19	16.8	76.4	606	13	US-10-027-632-69617	Sequence 69617, A
20	16.8	76.4	606	13	US-10-027-632-294476	Sequence 294476, A
21	16.8	76.4	606	13	US-10-027-632-294477	Sequence 294477, A
22	16.8	76.4	606	13	US-10-027-632-294477	Sequence 294477, A
23	16.8	76.4	606	15	US-10-027-632-69617	Sequence 69617, A
24	16.8	76.4	606	15	US-10-027-632-69618	Sequence 69618, A
25	16.8	76.4	606	15	US-10-027-632-294476	Sequence 294476, A
26	16.8	76.4	606	15	US-10-027-632-294477	Sequence 294477, A
27	16.8	76.4	632	18	US-10-425-115-51727	Sequence 51727, A
28	16.8	76.4	707	13	US-10-027-632-243832	Sequence 243832, A
29	16.8	76.4	707	13	US-10-027-632-243833	Sequence 243833, A
30	16.8	76.4	707	13	US-10-027-632-243834	Sequence 243834, A
31	16.8	76.4	707	15	US-10-027-632-243832	Sequence 243832, A
32	16.8	76.4	707	15	US-10-027-632-243833	Sequence 243833, A
33	16.8	76.4	729	13	US-10-027-632-243834	Sequence 243834, A
34	16.8	76.4	729	13	US-10-027-632-26514	Sequence 26514, A
35	16.8	76.4	729	13	US-10-027-632-26515	Sequence 26515, A
36	16.8	76.4	729	15	US-10-027-632-26514	Sequence 26514, A
37	16.8	76.4	729	15	US-10-027-632-26515	Sequence 26515, A
38	16.8	76.4	2167	15	US-10-106-698-1522	Sequence 1522, Ap
39	16.8	76.4	2502	16	US-10-424-599-13260	Sequence 13260, A
40	16.8	76.4	3242	16	US-10-108-260A-1314	Sequence 1314, Ap
41	16.8	76.4	31834	9	US-09-764-847-1612	Sequence 1612, Ap
42	16.8	76.4	31834	14	US-10-092-154-1612	Sequence 1612, Ap
43	16.8	76.4	32035	9	US-09-764-847-1611	Sequence 1611, Ap
44	16.8	76.4	32035	14	US-10-092-154-1611	Sequence 1611, Ap
45	16.4	74.5	568	17	US-10-437-963-16133	Sequence 16133, A

ALIGNMENTS

RESULT 1
US-09-943-115A-1
; Sequence 1, Application US/09943115A
; Publication No. US20030017469A1
; GENERAL INFORMATION:
; APPLICANT: SEQUENOM, Inc.
; APPLICANT: Rinsinger, Carl
; APPLICANT: Andersson, Maria
; APPLICANT: Lewander, Tommy
; APPLICANT: Olafsson, Erik
; TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9
; TITLE OF INVENTION: POLYMORPHISMS
; FILE REFERENCE: 52459-20021.00
; CURRENT FILING DATE: US/09/943, 115A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: UK 0021286.0
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-943-115A-1
Query Match 100.0%; Score 22; DB 10; Length 1345;
Best local Similarity 100.0%; Pred. No. 2,6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cyt 1 ATCTGTAGCTGTGCTGTGCTGTG 22
Db 745 ATCTGTAGCTGTGCTGTGCTGTG 766
RESULT 2

US-10-146-575-3
; Sequence 3, Application US/10146575
; Publication No. US20030059800A1
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/10/146,575
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US/09/144,367
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0)...(0)
US-10-146-575-3

Query Match 100.0%; Score 22; DB 14; Length 1345;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATCTGTAGTGTGGCTTGTGG 22
|||
Db 745 ATCTGTAGTGTGGCTTGTGG 766

RESULT 3
US-10-085-612-3
; Sequence 3, Application US/10085612
; Publication No. US20030096251A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Vredenburg, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Marks, Jeffrey
; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
; FILE REFERENCE: 4389-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-612-3

Query Match 100.0%; Score 22; DB 14; Length 1345;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATCTGTAGTGTGGCTTGTGG 22
|||
Db 745 ATCTGTAGTGTGGCTTGTGG 766

RESULT 4
US-10-121-960C-14
; Sequence 14, Application US/10121960C
; Publication No. US20030145341A1

; GENERAL INFORMATION:
; APPLICANT: ZHANG, Weisheng
; APPLICANT: CONTAG, Pamela
; APPLICANT: PURCHIO, Anthony
; APPLICANT: HASHIMA, Sandy
; APPLICANT: MA, Shitley
; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
; TITLE OF INVENTION: TRANSCRIPTION CONTROL ELEMENTS ASSOCIATED WITH
; FILE REFERENCE: 9400-0014 / PXE-014.US
; CURRENT APPLICATION NUMBER: US/10/121,960C
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 13035
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human CYP3A4 gene locus
US-10-121-960C-14

Query Match 100.0%; Score 22; DB 15; Length 13035;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATCTGTAGTGTGGCTTGTGG 22
|||
Db 12570 ATCTGTAGTGTGGCTTGTGG 12591

RESULT 5
US-10-121-960C-17
; Sequence 17, Application US/10121960C
; Publication No. US20030145341A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, Weisheng
; APPLICANT: CONTAG, Pamela
; APPLICANT: PURCHIO, Anthony
; APPLICANT: HASHIMA, Sandy
; APPLICANT: MA, Shitley
; APPLICANT: NAMOTKA, Kevin
; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
; TITLE OF INVENTION: TRANSCRIPTION CONTROL ELEMENTS ASSOCIATED WITH
; FILE REFERENCE: 9400-0014 / PXE-014.US
; CURRENT APPLICATION NUMBER: US/10/121,960C
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 15185
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CYP3A4-luc transgene
US-10-121-960C-17

Query Match 100.0%; Score 22; DB 15; Length 15185;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATCTGTAGTGTGGCTTGTGG 22
|||
Db 12570 ATCTGTAGTGTGGCTTGTGG 12591

RESULT 6
US-10-114-908-9
; Sequence 9, Application US/10114908
; Publication No. US20040229222A1
; GENERAL INFORMATION:

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; APPLICANT: Luehreen, Kenneth R.
; TITLE OF INVENTION: P450 Single Nucleotide Polymorphism Biochip Analysis
; FILE REFERENCE: A-70398-1/RMS/DIR
; CURRENT APPLICATION NUMBER: US/10/114,908
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 60/280,583
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 277
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-114-908-9

Query Match      90.9%; Score 20; DB 18; Length 26;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 CTGAGGTGGCTGTTGG 22
Db      1 CTGAGGTGGCTGTTGG 20

RESULT 7
US-10-085-117-235
; Sequence 235, Application US/10085117
; Publication No. US20030232334A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 235
; LENGTH: 33488
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)...(33488)
; OTHER INFORMATION: n = any nucleotide
; US-10-085-117-235

Query Match      88.2%; Score 19.4; DB 15; Length 33488;
Best Local Similarity 95.2%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ATCTGAGTGTGGCTTGTG 21
Db      1609 ATCTGATGTGTGGCTTGTG 1629

RESULT 8
US-09-957-997-4
; Sequence 4, Application US/09957997
; Patent No. US20020150915A1
; GENERAL INFORMATION:
; APPLICANT: Berkenstam, Anders
; APPLICANT: Bertilsson, Gran
; APPLICANT: Blomquist, Patrik
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-046001
; CURRENT APPLICATION NUMBER: US/09/957,997
; CURRENT FILING DATE: 2001-09-21
; EARLIER APPLICATION NUMBER: SE 0003393-6
; EARLIER FILING DATE: 2000-09-22
; EARLIER APPLICATION NUMBER: 60/238,895
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; EARLIER FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1012
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-957-997-4

Query Match      85.5%; Score 18.8; DB 9; Length 1012;
Best Local Similarity 90.9%; Pred. No. 74;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ATCTGAGTGTGGCTTGTG 22
Db      668 ATCTGAGCATGGCTTGTG 689

RESULT 9
US-09-070-927A-78
; Sequence 78, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunach
; APPLICANT: Patrick J. Dillon
; APPLICANT: Steven Barash
; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 982
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,927A
; FILING DATE: 04-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7053 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-09-070-927A-78

Query Match      85.5%; Score 18.8; DB 9; Length 7053;
Best Local Similarity 90.9%; Pred. No. 79;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ATCTGAGTGTGGCTTGTG 22
```

Db 835 ATCTGAAGTGTGCTTTGG 856

RESULT 10

US-09-957-997-1

; Sequence 1, Application US/09957997
; Patent No. US20020150915A1

; GENERAL INFORMATION:

; APPLICANT: Berkenstam, Anders

; APPLICANT: Berkenstam, Anders

; APPLICANT: Blomquist, Patrik

; TITLE OF INVENTION: PROMOTER SEQUENCES

; FILE REFERENCE: 13425-046001

; CURRENT APPLICATION NUMBER: US/09/957,997

; CURRENT FILING DATE: 2001-09-21

; EARLIER APPLICATION NUMBER: SE 0003393-6

; EARLIER FILING DATE: 2000-09-22

; EARLIER APPLICATION NUMBER: 60/238,895

; EARLIER FILING DATE: 2000-10-10

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 11186

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-957-997-1

Query Match 85.5%; Score 18.8; DB 9; Length 11186;

Best Local Similarity 90.9%; Pred. No. 80;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATCTGAGTGTGCTTTGG 22

Db 10785 ATCTGAGTGTGCTTTGG 10806

RESULT 11

US-09-820-893-28

; Sequence 28, Application US/09820893

; Patent No. US20020076705A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 31 Human Secreted Proteins

; FILE REFERENCE: P2033P1

; CURRENT APPLICATION NUMBER: US/09/820,893

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: 09/531,119

; PRIOR FILING DATE: 2000-03-20

; PRIOR APPLICATION NUMBER: 60/102,895

; PRIOR FILING DATE: 1998-10-02

; NUMBER OF SEQ ID NOS: 140

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 28

; LENGTH: 1378

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-820-893-28

Query Match 80.9%; Score 17.8; DB 9; Length 1378;

Best Local Similarity 90.5%; Pred. No. 2.1e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCTGTAGTGTGCTTTGG 22

Db 417 TCTGTAGTGTGCTTTGG 437

RESULT 12

US-10-607-565-28

; Sequence 28, Application US/10607565

; Publication No. US20040048294A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 31 Human Secreted Proteins

; FILE REFERENCE: P2033P1

; CURRENT APPLICATION NUMBER: US/10/607,565

; CURRENT FILING DATE: 2003-06-27

; PRIOR APPLICATION NUMBER: US/09/531,119

; PRIOR FILING DATE: 2000-03-20

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/101,546

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/102,895

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-02

; NUMBER OF SEQ ID NOS: 140

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 28

; LENGTH: 1378

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-607-565-28

Query Match 80.9%; Score 17.8; DB 16; Length 1378;

Best Local Similarity 90.5%; Pred. No. 2.1e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCTGTAGTGTGCTTTGG 22

Db 417 TCTGTAGTGTGCTTTGG 437

RESULT 13

US-10-425-115-172581

; Sequence 172581, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 172581

; LENGTH: 615

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_88977C.1

US-10-425-115-172581

Query Match 78.2%; Score 17.2; DB 18; Length 615;

Best Local Similarity 86.4%; Pred. No. 3.9e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATCTGAGTGTGCTTTGG 22

Db 527 AGCTGAGTGTGCTTTGG 548

RESULT 14

US-10-085-612-4

; Sequence 4, Application US/10085612

; Publication No. US20030096251A1

; GENERAL INFORMATION:

; APPLICANT: Guida, Marco

; APPLICANT: Hall, Jeff

; APPLICANT: Petros, William

; APPLICANT: Vredenburg, James

; APPLICANT: Colvin, Oliver

; APPLICANT: Marks, Jeffrey

; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals

; FILE REFERENCE: 4389-5-C1

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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 11:30:01 ; Search time 32.8 Seconds
(without alignments)
520.089 Million cell updates/sec

Title: US-10-085-612a-18

Perfect score: 24
Sequence: 1 taccagaactcaagtgagccat 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	24	100.0	1345	US-09-372-339-1	Sequence 1, Appli
C 2	24	100.0	1345	US-09-372-339-2	Sequence 2, Appli
C 3	24	100.0	1345	US-09-144-367-3	Sequence 3, Appli
C 4	16.8	70.0	588	US-08-248-786A-2251	Sequence 2251, Ap
C 5	16.6	69.2	495	US-08-222-719-6	Sequence 6, Appli
C 6	16.6	69.2	495	US-08-470-925-6	Sequence 6, Appli
C 7	16.6	69.2	495	US-08-471-613-6	Sequence 6, Appli
C 8	16.6	69.2	495	PCT-US93-10443-6	Sequence 6, Appli
C 9	16.6	69.2	7815	US-09-102-528-28	Sequence 28, Appli
C 10	16.2	67.5	482	US-09-621-976-13491	Sequence 13491, A
C 11	16.2	67.5	9626	US-09-150-867-2	Sequence 2, Appli
C 12	16	66.7	374	US-09-621-976-18735	Sequence 18735, A
C 13	16	66.7	406	US-09-621-976-18740	Sequence 18740, A
C 14	16	66.7	479	US-09-621-976-2114	Sequence 2114, Ap
C 15	16	66.7	666	US-09-543-681A-81	Sequence 81, Appli
C 16	16	66.7	783	US-08-181-271A-34	Sequence 34, Appli
C 17	16	66.7	783	US-08-449-315-34	Sequence 34, Appli
C 18	16	66.7	783	US-08-444-803-34	Sequence 34, Appli
C 19	16	66.7	783	US-08-449-043-34	Sequence 34, Appli
C 20	16	66.7	783	US-08-456-265A-34	Sequence 34, Appli
C 21	16	66.7	783	US-08-455-416-34	Sequence 34, Appli
C 22	16	66.7	783	US-08-455-244-34	Sequence 34, Appli
C 23	16	66.7	783	US-08-454-876-34	Sequence 34, Appli
C 24	16	66.7	783	US-08-457-364-34	Sequence 34, Appli
C 25	16	66.7	783	US-08-456-262-34	Sequence 34, Appli
C 26	16	66.7	783	US-08-456-240-34	Sequence 34, Appli
C 27	16	66.7	783	US-08-455-736-34	Sequence 34, Appli

C 28	16	66.7	783	US-08-971-217-34	Sequence 34, Appli
C 29	16	66.7	783	US-09-350-600-34	Sequence 34, Appli
C 30	16	66.7	783	US-09-906-234-34	Sequence 34, Appli
C 31	16	66.7	1792	US-09-205-258-34	Sequence 34, Appli
C 32	16	66.7	1998	US-09-248-796A-3079	Sequence 3079, Ap
C 33	16	66.7	580073	US-08-545-528D-1	Sequence 1, Appli
C 34	15.8	65.8	28	US-07-786-902-3	Sequence 3, Appli
C 35	15.8	65.8	800	US-08-998-416-334	Sequence 334, App
C 36	15.8	65.8	879	US-09-976-594-987	Sequence 987, App
C 37	15.8	65.8	14636	US-09-173-814-6	Sequence 6, Appli
C 38	15.8	65.8	118067	US-09-497-855A-32	Sequence 32, Appli
C 39	15.6	65.0	100	US-09-513-999C-14370	Sequence 14370, A
C 40	15.6	65.0	219	US-09-134-000C-449	Sequence 449, App
C 41	15.6	65.0	334	US-09-513-999C-2677	Sequence 2677, Ap
C 42	15.6	65.0	408	US-09-270-767-3057	Sequence 3057, Ap
C 43	15.6	65.0	408	US-09-270-767-18339	Sequence 18339, A
C 44	15.6	65.0	456	US-09-513-999C-11915	Sequence 11915, A
C 45	15.6	65.0	514	US-09-621-976-2275	Sequence 2275, Ap

ALIGNMENTS

RESULT 1
US-09-372-339-1/c
Sequence 1, Application US/09372339
Patent No. 6174684
GENERAL INFORMATION:
APPLICANT: Redbeck, Timothy
APPLICANT: Felix, Carolyn
TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
FILE REFERENCE: PENN-0695
CURRENT APPLICATION NUMBER: US/09/372,339
CURRENT FILING DATE: 1999-08-11
EARLIER APPLICATION NUMBER: 60/096,586
EARLIER FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 1
LENGTH: 1345
TYPE: DNA
ORGANISM: Homo sapiens
US-09-372-339-1

Query Match 100.0%; Score 24; DB 3; Length 1345;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TATCAGAACTCAAGTGAGCCAT 24
870 TATCAGAACTCAAGTGAGCCAT 847

RESULT 2
US-09-372-339-2/c
Sequence 2, Application US/09372339
Patent No. 6174684
GENERAL INFORMATION:
APPLICANT: Redbeck, Timothy
APPLICANT: Felix, Carolyn
TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
FILE REFERENCE: PENN-0695
CURRENT APPLICATION NUMBER: US/09/372,339
CURRENT FILING DATE: 1999-08-11
EARLIER APPLICATION NUMBER: 60/096,586
EARLIER FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 2
LENGTH: 1345
TYPE: DNA
ORGANISM: Homo sapiens
US-09-372-339-2

Query Match 100.0%; Score 24; DB 3; Length 1345;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATCAGAACTCAAGTGAGCCAT 24
Db 870 TATCAGAACTCAAGTGAGCCAT 847

RESULT 3

US-09-144-367-3/C
; Sequence 3, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Guido, Jay
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0) ... (0)
US-09-144-367-3

Query Match 100.0%; Score 24; DB 4; Length 1345;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATCAGAACTCAAGTGAGCCAT 24
Db 870 TATCAGAACTCAAGTGAGCCAT 847

RESULT 4

US-09-248-796A-2251
; Sequence 2251, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 2251
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-2251

Query Match 70.0%; Score 16.8; DB 4; Length 588;
Best Local Similarity 90.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ATCAGAACTCAAGTGAGGC 21
Db 172 ATCAGAACTCAATTGATC 191

RESULT 5
US-08-222-719-6
; Sequence 6, Application US/08222719
; Patent No. 5846711
; GENERAL INFORMATION:
; APPLICANT: David D. Moore
; TITLE OF INVENTION: NUCLEAR HORMONE RECEPTOR-
; TITLE OF INVENTION: INTERACTING POLYPEPTIDES AND
; TITLE OF INVENTION: RELATED MOLECULES AND METHODS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,719
FILING DATE: 04-April-1994
CLASSIFICATION: 436

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959,136
FILING DATE: 30-October-1992
CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark

REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/229001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906

TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 495
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-08-222-719-6

Query Match 69.2%; Score 16.6; DB 2; Length 495;
Best Local Similarity 82.6%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ATCAGAACTCAAGTGAGCCAT 24
Db 379 ATCAGAAATTAAGTCGAGCAAT 401

RESULT 6

US-08-470-925-6
; Sequence 6, Application US/08470925
; Patent No. 5866886
; GENERAL INFORMATION:
; APPLICANT: David D. Moore
; APPLICANT: Jae Moon Lee
; TITLE OF INVENTION: NUCLEAR HORMONE RECEPTOR-
; TITLE OF INVENTION: INTERACTING POLYPEPTIDES AND
; TITLE OF INVENTION: RELATED MOLECULES AND METHODS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts

COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,925
FILING DATE: 06-June-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222,719
FILING DATE: 04-April-1994
CLASSIFICATION: 435
APPLICATION NUMBER: 07/969,136
FILING DATE: October 30, 1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/229003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 495
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-470-925-6

Query Match 69.2%; Score 16.6; DB 2; Length 495;
Best Local Similarity 82.6%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATCAGAACTCAAGTGAGCCAT 24
DB 379 ATCAGAAATTAACTGACGCAAT 401

RESULT 7
US-08-471-613-6
Sequence 6, Application US/08471613
Patent No. 5962256
GENERAL INFORMATION:
APPLICANT: David D. Moore
APPLICANT: Jae Moon Lee
TITLE OF INVENTION: NUCLEAR HORMONE RECEPTOR-
INTERACTING POLYPEPTIDES AND
TITLE OF INVENTION: RELATED MOLECULES AND METHODS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,613
FILING DATE: 06-June-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222,719
FILING DATE: 04-April-1994

CLASSIFICATION: 436
APPLICATION NUMBER: 07/969,136
FILING DATE: October 30, 1992
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/229001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 495
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-471-613-6

Query Match 69.2%; Score 16.6; DB 2; Length 495;
Best Local Similarity 82.6%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATCAGAACTCAAGTGAGCCAT 24
DB 379 ATCAGAAATTAACTGACGCAAT 401

RESULT 8
PCT-US93-10443-6
Sequence 6, Application PC/TUS9310443
GENERAL INFORMATION:
APPLICANT: David D. Moore
APPLICANT: Jae W. Lee
TITLE OF INVENTION: NUCLEAR HORMONE RECEPTOR-
INTERACTING POLYPEPTIDES AND
TITLE OF INVENTION: RELATED MOLECULES AND METHODS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10443
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,136
FILING DATE: October 30, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/099002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 495
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
PCT-US93-10443-6

Query Match 69.2%; Score 16.6; DB 5; Length 495;
Best Local Similarity 82.6%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATCAGAACTCAAGTGCAGCCAT 24
|||||
Db 379 ATCAGAAATTAAGTGCAGCAT 401

RESULT 9
US-09-102-528-28/C
; Sequence 28, Application US/09102528
; Patent No. 6207883
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA Sequences
; NUMBER OF SEQUENCES: 32
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (ERO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,528
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB96/03191
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7815 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-102-528-28

Query Match 69.2%; Score 16.6; DB 3; Length 7815;
Best Local Similarity 82.6%; Pred. No. 95;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATCAGAACTCAAGTGCAGCCAT 24
|||||
Db 386 ATCAGCACTGAAGTGCAGCCAT 3846

RESULT 10
US-09-621-976-13491/C
; Sequence 13491, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13491
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-13491

Query Match 67.5%; Score 16.2; DB 4; Length 482;
Best Local Similarity 85.7%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TCAGAACTCAAGTGCAGCCA 23
|||||

Db 276 TCAGAGACTCAAGTGCAGCCA 256

RESULT 11
US-09-150-867-2
; Sequence 2, Application US/09150867
; Patent No. 6645748
; GENERAL INFORMATION:
; APPLICANT: Wood, Kenneth W.
; APPLICANT: Sakowicz, Roman
; APPLICANT: Goldstein, Lawrence S.B.
; APPLICANT: Cleveland, Don W.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Plus End-Directed Microtubule Motor Required for
; FILE REFERENCE: 18557C-000110US
; CURRENT APPLICATION NUMBER: US/09/150,867
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: US 60/058,645
; EARLIER FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 9626
; TYPE: DNA
; ORGANISM: Xenopus sp.
; FEATURE:
; OTHER INFORMATION: XCENP-B nucleotide sequence
; NAME/KEY: CDS
; LOCATION: (143)..(9007)
US-09-150-867-2

Query Match 67.5%; Score 16.2; DB 4; Length 9626;
Best Local Similarity 85.7%; Pred. No. 1,6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATCAGAACTCAAGTGCAGC 21
|||||
Db 3301 TATCAGAAACAAAGTCAAGC 3321

RESULT 12
US-09-621-976-18735
; Sequence 18735, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 18735
; LENGTH: 374
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-18735

Query Match 66.7%; Score 16; DB 4; Length 374;
Best Local Similarity 79.2%; Pred. No. 97;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TATCAGAACTCAAGTGCAGCCAT 24
|||||
Db 172 TACGAGCACACATTTGAAGCCAT 195

RESULT 13
US-09-621-976-18740

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; Sequence 18740, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 18740
; LENGTH: 406
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-18740
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Query Match          66.7%; Score 16; DB 4; Length 406;
Best Local Similarity 79.2%; Pred. No. 99;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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```
QY      1 TATCAGAACTCAAGTGAGCCAT 24
Db      172 TAGCAGACACCAATTGAGCCAT 195
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```
RESULT 14
US-09-621-976-2114
; Sequence 2114, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2114
; LENGTH: 479
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: 125..322
US-09-621-976-2114
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Query Match          66.7%; Score 16; DB 4; Length 479;
Best Local Similarity 79.2%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY      1 TATCAGAACTCAAGTGAGCCAT 24
Db      442 TGTCAAACTCAAAAGAAATCAT 465
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RESULT 15
US-09-543-681A-81
; Sequence 81, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543.681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
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; SEQ ID NO 81
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-81
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Query Match          66.7%; Score 16; DB 4; Length 666;
Best Local Similarity 79.2%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY      1 TATCAGAACTCAAGTGAGCCAT 24
Db      308 TATCGAGCCTCAAGTAGCGCCAT 331
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Search completed: January 26, 2005, 13:15:21
Job time : 33.925 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 13:15:32 ; Search time 170.133 Seconds
(without alignments)
810.549 Million cell updates/sec

Title: US-10-085-612A-18

Perfect score: 24

Sequence: 1 taccagaactcaagtcgagccat 24

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	24	100.0	1345	10	US-09-943-115A-1
C 2	24	100.0	1345	14	US-10-146-575-3
C 3	24	100.0	1345	14	US-10-085-612-3
C 4	24	100.0	13035	15	US-10-121-960C-14
C 5	24	100.0	15185	15	US-10-121-960C-17
C 6	22.4	93.3	1012	9	US-09-957-997-4
C 7	22.4	93.3	1254	14	US-10-085-612-4
C 8	22.4	93.3	1186	9	US-09-957-997-1
C 9	18.8	78.3	188	9	US-09-783-550-11156
C 10	18.4	76.7	673	18	US-10-653-047-6542
C 11	17.8	74.2	456	17	US-10-437-963-48048
C 12	17.8	74.2	556	9	US-09-917-800A-985

C 13	17.8	74.2	2724	17	US-10-437-963-48046	Sequence 48046, A
C 14	17.6	73.3	4042	15	US-10-128-714-347	Sequence 347, App
C 15	17.6	73.3	4043	15	US-10-128-714-5347	Sequence 5347, Ap
C 16	17.4	72.5	276	9	US-09-864-761-18789	Sequence 18789, A
C 17	17.4	72.5	465	9	US-09-864-761-2044	Sequence 2044, Ap
C 18	17.4	72.5	636	13	US-10-027-632-264198	Sequence 264198, A
C 19	17.4	72.5	636	15	US-10-027-632-264198	Sequence 191, App
C 20	17.2	71.7	398	10	US-09-854-867-191	Sequence 264198, A
C 21	17.2	71.7	490	15	US-10-102-524-504	Sequence 504, App
C 22	17.2	71.7	517	13	US-10-027-632-77419	Sequence 77419, A
C 23	17.2	71.7	517	13	US-10-027-632-314056	Sequence 314056, A
C 24	17.2	71.7	517	15	US-10-027-632-314056	Sequence 77419, A
C 25	17.2	71.7	517	15	US-10-027-632-314056	Sequence 314056, A
C 26	17.2	71.7	532	13	US-10-102-524-1796	Sequence 1796, Ap
C 27	17.2	71.7	615	15	US-10-027-632-225776	Sequence 225776, A
C 28	17.2	71.7	615	15	US-10-027-632-225776	Sequence 225776, A
C 29	17.2	71.7	628	18	US-10-425-115-60396	Sequence 60396, A
C 30	17.2	71.7	673	13	US-10-027-632-219635	Sequence 219635, A
C 31	17.2	71.7	673	13	US-10-027-632-219635	Sequence 219635, A
C 32	17.2	71.7	673	13	US-10-027-632-219637	Sequence 219637, A
C 33	17.2	71.7	673	15	US-10-027-632-219635	Sequence 219635, A
C 34	17.2	71.7	673	15	US-10-027-632-219637	Sequence 219637, A
C 35	17.2	71.7	673	15	US-10-027-632-219637	Sequence 219637, A
C 36	17.2	71.7	1238	16	US-10-424-599-12818	Sequence 12818, A
C 37	17.2	71.7	1281	16	US-10-424-599-12818	Sequence 43984, A
C 38	17.2	71.7	1370	18	US-10-739-930-4661	Sequence 4661, Ap
C 39	16.8	70.0	410	10	US-09-918-995-12886	Sequence 22886, A
C 40	16.8	70.0	534	15	US-10-029-386-9254	Sequence 9254, Ap
C 41	16.8	70.0	549	9	US-09-867-550-1091	Sequence 1091, Ap
C 42	16.8	70.0	584	13	US-10-027-632-186339	Sequence 186339, A
C 43	16.8	70.0	584	13	US-10-027-632-186340	Sequence 186340, A
C 44	16.8	70.0	584	15	US-10-027-632-186339	Sequence 186339, A
C 45	16.8	70.0	584	15	US-10-027-632-186340	Sequence 186340, A

ALIGNMENTS

RESULT 1
US-09-943-115A-1/c
Sequence 1, Application US/09943115A
Publication No. US20030017469A1
GENERAL INFORMATION:
APPLICANT: SEQUENOM, Inc.
APPLICANT: Rieinger, Carl
APPLICANT: Anderson, Maria
APPLICANT: Lewander, Tommy
APPLICANT: Olaisson, Erik
TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9
FILE REFERENCE: 52459-20021.00
CURRENT APPLICATION NUMBER: US/09/943.115A
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: UK 0021286.0
PRIOR FILING DATE: 2000-08-30
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1345
TYPE: DNA
ORGANISM: Homo sapiens
US-09-943-115A-1

Query Match 100.0%; Score 24; DB 10; Length 1345;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 TATCAGAAGCTCAAGTCGAGCCAT 24
Db 870 TATCAGAAGCTCAAGTCGAGCCAT 847

RESULT 2

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US-10-146-575-3/c
; Sequence 3, Application US/10146575
; Publication No. US20030059800A1
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/10/146, 575
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US/09/144,367
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0)...(0)
US-10-146-575-3
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Query Match      100.0%; Score 24; DB 14; Length 1345;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 TATCAGAACTCAAGTGGAGCCAT 24
Db      870 TATCAGAACTCAAGTGGAGCCAT 847
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RESULT 3
US-10-085-612-3/c
; Sequence 3, Application US/10085612
; Publication No. US20030096251A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Vredenburgh, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Marks, Jeffrey
; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
; FILE REFERENCE: 4389-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-612-3
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Query Match      100.0%; Score 24; DB 14; Length 1345;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 TATCAGAACTCAAGTGGAGCCAT 24
Db      870 TATCAGAACTCAAGTGGAGCCAT 847
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RESULT 4
US-10-121-960C-14/c
; Sequence 14, Application US/10121960C
; Publication No. US20030145341A1
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; GENERAL INFORMATION:
; APPLICANT: ZHANG, Weisheng
; APPLICANT: CONTAG, Pamela
; APPLICANT: PURCHIO, Anthony
; APPLICANT: HASHIMA, Sandy
; APPLICANT: MA, Shirley
; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
; TITLE OF INVENTION: TRANSCRIPTION CONTROL ELEMENTS ASSOCIATED WITH
; FILE REFERENCE: 9400-0014 / PXE-014.US
; CURRENT APPLICATION NUMBER: US/10/121,960C
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 13035
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human CYP3A4 gene locus
US-10-121-960C-14
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Query Match      100.0%; Score 24; DB 15; Length 13035;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 TATCAGAACTCAAGTGGAGCCAT 24
Db      12695 TATCAGAACTCAAGTGGAGCCAT 12672
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```
RESULT 5
US-10-121-960C-17/c
; Sequence 17, Application US/10121960C
; Publication No. US20030145341A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, Weisheng
; APPLICANT: CONTAG, Pamela
; APPLICANT: PURCHIO, Anthony
; APPLICANT: HASHIMA, Sandy
; APPLICANT: MA, Shirley
; APPLICANT: NAMOTKA, Kevin
; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
; TITLE OF INVENTION: TRANSCRIPTION CONTROL ELEMENTS ASSOCIATED WITH
; FILE REFERENCE: 9400-0014 / PXE-014.US
; CURRENT APPLICATION NUMBER: US/10/121,960C
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 15185
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CYP3A4-luc transgene
US-10-121-960C-17
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Query Match      100.0%; Score 24; DB 15; Length 15185;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 TATCAGAACTCAAGTGGAGCCAT 24
Db      12695 TATCAGAACTCAAGTGGAGCCAT 12672
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```
RESULT 6
US-09-957-997-4/c
; Sequence 4, Application US/09957997
; Patent No. US20020150915A1
; GENERAL INFORMATION:
```


APPLICANT: Berkenstam, Anders
APPLICANT: Bertilsson, Gran
APPLICANT: Blomquist, Patrik
TITLE OF INVENTION: PROMOTER SEQUENCES
FILE REFERENCE: 13425-046001
CURRENT APPLICATION NUMBER: US/09/957,997
CURRENT FILING DATE: 2001-09-21
EARLIER APPLICATION NUMBER: SE 0003393-6
EARLIER FILING DATE: 2000-09-22
EARLIER APPLICATION NUMBER: 60/238,895
EARLIER FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1012
TYPE: DNA
ORGANISM: Homo sapiens
US-09-957-997-4

Query Match 93.3%; Score 22.4; DB 9; Length 1012;
Best Local Similarity 95.8%; Pred. No. 0.97;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TATCAGAACTCAAGTGAGCCAT 24
Db 783 TATCAGAACTCAAGTGAGCCAT 760

RESULT 7
US-10-085-612-4/c
Sequence 4, Application US/10085612
Publication No. US20030096251A1
GENERAL INFORMATION:

APPLICANT: Guida, Marco
APPLICANT: Hall, Jeff
APPLICANT: Petros, William
APPLICANT: Vredenburg, James
APPLICANT: Colvin, Oliver
APPLICANT: Marks, Jeffrey
TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
FILE REFERENCE: 4389-5-C1
CURRENT APPLICATION NUMBER: US/10/085,612
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/144,367
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/271,630
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 1254
TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-612-4

Query Match 93.3%; Score 22.4; DB 14; Length 1254;
Best Local Similarity 95.8%; Pred. No. 1;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TATCAGAACTCAAGTGAGCCAT 24
Db 905 TATCAGAACTCAAGTGAGCCAT 882

RESULT 8
US-09-957-997-1/c
Sequence 1, Application US/09957997
Patent No. US20020150915A1
GENERAL INFORMATION:
APPLICANT: Berkenstam, Anders
APPLICANT: Bertilsson, Gran
APPLICANT: Blomquist, Patrik

TITLE OF INVENTION: PROMOTER SEQUENCES
FILE REFERENCE: 13425-046001
CURRENT APPLICATION NUMBER: US/09/957,997
CURRENT FILING DATE: 2001-09-21
EARLIER APPLICATION NUMBER: SE 0003393-6
EARLIER FILING DATE: 2000-09-22
EARLIER APPLICATION NUMBER: 60/238,895
EARLIER FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1186
TYPE: DNA
ORGANISM: Homo sapiens
US-09-957-997-1

Query Match 93.3%; Score 22.4; DB 9; Length 1186;
Best Local Similarity 95.8%; Pred. No. 1.4;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TATCAGAACTCAAGTGAGCCAT 24
Db 10900 TATCAGAACTCAAGTGAGCCAT 10877

RESULT 9
US-09-783-590-11156
Sequence 11156, Application US/09783590
Patent No. US20020110850A1
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven W.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16,2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11156
LENGTH: 188
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (52)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (66)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (85)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (133)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (176)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (188)
OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-11156

Query Match 78.3%; Score 18.8; DB 9; Length 188;
Best Local Similarity 87.0%; Pred. No. 43;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Mu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 48046
LENGTH: 2724
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_50759C.1
US-10-437-963-48046

Query Match 74.2%; Score 17.8; DB 17; Length 2724;
Best Local Similarity 90.5%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 2;

QY 4 CAGAACTCAAGTGCAGCCAT 24
DB 2537 CAGAACTCAAGTGCAGCCAT 2557

RESULT 14
US-10-128-714-347/C
Sequence 347, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Erosbkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 347
LENGTH: 4042
TYPE: DNA
ORGANISM: Aspergillus fumigatus
US-10-128-714-347

Query Match 73.3%; Score 17.6; DB 15; Length 4042;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TATCAGAACTCAAGTGCAGCCAT 24
DB 3941 TATCAGAACTCAAGTGCAGCCAT 3918

RESULT 15

US-10-128-714-5347/C
Sequence 5347, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Erosbkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5347
LENGTH: 4043
TYPE: DNA
ORGANISM: Aspergillus fumigatus
US-10-128-714-5347

Query Match 73.3%; Score 17.6; DB 15; Length 4043;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TATCAGAACTCAAGTGCAGCCAT 24
DB 3942 TATCAGAACTCAAGTGCAGCCAT 3919

Search completed: January 26, 2005, 18:15:47
Job time: 171.133 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 11:30:01 ; Search time 25.9667 Seconds
(without alignments)
520.089 Million cell updates/sec

Title: US-10-085-612A-21

Sequence: 1 ggcgtgtgcgtatcttgc 19

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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- 6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	16.4	86.3	1345	3	US-09-372-339-1	Sequence 1, Appli
2	16.4	86.3	1345	3	US-09-372-339-2	Sequence 2, Appli
3	16.4	86.3	1345	4	US-09-144-367-3	Sequence 3, Appli
4	15.8	83.2	5722	4	US-09-566-921-54	Sequence 54, Appl
5	15.8	83.2	5722	4	US-09-919-039-174	Sequence 174, App
6	14.8	77.9	1332	4	US-09-513-999C-16924	Sequence 16924, A
7	14.8	77.9	402	4	US-09-513-999C-16738	Sequence 16738, A
8	14.8	77.9	1617	2	US-08-540-118-2	Sequence 2, Appli
9	14.8	77.9	1617	4	US-09-185-818-2	Sequence 2, Appli
10	14.8	77.9	49312	4	US-09-671-317-485	Sequence 485, App
11	14.4	75.8	250	4	US-09-513-999C-18974	Sequence 18974, A
12	14.4	75.8	451	4	US-09-702-705-1647	Sequence 1647, Ap
13	14.4	75.8	451	4	US-09-736-457-1647	Sequence 1647, Ap
14	14.4	75.8	451	4	US-09-614-124B-1647	Sequence 1647, Ap
15	14.4	75.8	451	4	US-09-671-325-1647	Sequence 1647, Ap
16	14.4	75.8	451	4	US-09-658-824-1647	Sequence 1647, Ap
17	14.4	75.8	2820	4	US-09-540-236-479	Sequence 479, App
18	14.4	75.8	2932	3	US-08-999-774A-5	Sequence 5, Appli
19	14.4	75.8	2933	4	US-09-149-476-165	Sequence 165, App
20	14.4	75.8	3276	4	US-09-149-476-298	Sequence 298, App
21	14.4	75.8	3447	4	US-09-221-017B-816	Sequence 816, App
22	14.4	75.8	3768	4	US-09-566-921-50	Sequence 50, Appl
23	14.4	75.8	41684	4	US-09-536-059-1	Sequence 1, Appli
24	14.4	75.8	65792	4	US-09-536-002-31	Sequence 31, Appli
25	14.4	75.8	162450	3	US-09-345-882-1	Sequence 1, Appli
26	14.2	74.7	67	4	US-08-956-171E-2676	Sequence 2676, Ap
27	14.2	74.7	67	4	US-08-761-986A-2676	Sequence 2676, Ap

28	14.2	74.7	378	4	US-09-702-705-1495	Sequence 1495, Ap
29	14.2	74.7	378	4	US-09-736-457-1495	Sequence 1495, Ap
30	14.2	74.7	378	4	US-09-614-124B-1495	Sequence 1495, Ap
31	14.2	74.7	378	4	US-09-671-325-1495	Sequence 1495, Ap
32	14.2	74.7	378	4	US-09-658-824-1495	Sequence 1495, Ap
33	14.2	74.7	393	4	US-09-134-000C-45	Sequence 45, Appl
34	14.2	74.7	407	4	US-09-401-064-174	Sequence 174, App
35	14.2	74.7	420	4	US-09-252-991A-6401	Sequence 6401, App
36	14.2	74.7	433	4	US-09-513-999C-1943	Sequence 1943, Ap
37	14.2	74.7	442	4	US-09-513-999C-9621	Sequence 9621, Ap
38	14.2	74.7	630	2	US-08-117-981-5	Sequence 5, Appli
39	14.2	74.7	630	2	US-08-477-081-5	Sequence 5, Appli
40	14.2	74.7	630	5	PCT-US93-02142-5	Sequence 5, Appli
41	14.2	74.7	705	4	US-09-107-532A-1163	Sequence 1163, Ap
42	14.2	74.7	756	4	US-09-270-767-88	Sequence 88, Appl
43	14.2	74.7	756	4	US-09-270-767-15370	Sequence 15370, A
44	14.2	74.7	845	1	US-08-589-446-3	Sequence 3, Appli
45	14.2	74.7	845	1	US-08-444-882-3	Sequence 3, Appli

ALIGNMENTS

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RESULT 1
US-09-372-339-1
; Sequence 1, Application US/09372339
; Patent No. 6174684
; GENERAL INFORMATION:
; APPLICANT: Redbeck, Timothy
; APPLICANT: Felix, Carolyn
; TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
; FILE REFERENCE: PNN-0695
; CURRENT FILING DATE: 1999-08-11
; EARLIER FILING DATE: 1999-08-11
; EARLIER APPLICATION NUMBER: 60/096,586
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-372-339-1

Query Match      86.3%; Score 16.4; DB 3; Length 1345;
Best Local Similarity 94.4%; Pred. No. 14;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      2 GTGTGTGCAATCTTTC 19
Db      963 GTGTGTGCAATCTTTC 980

RESULT 2
US-09-372-339-2
; Sequence 2, Application US/09372339
; Patent No. 6174684
; GENERAL INFORMATION:
; APPLICANT: Redbeck, Timothy
; APPLICANT: Felix, Carolyn
; TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
; FILE REFERENCE: PNN-0695
; CURRENT FILING DATE: 1999-08-11
; EARLIER FILING DATE: 1999-08-11
; EARLIER APPLICATION NUMBER: 60/096,586
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-372-339-2
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Query Match 86.3%; Score 16.4; DB 3; Length 1345;
Best Local Similarity 94.4%; Pred. No. 14;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTGTGTGCATCTTTGC 19
|||||
Db 963 GTGTGTGCATCTTTGC 980

RESULT 3
US-09-144-367-3
; Sequence 3, Application US/09144367
; Patent No. 632639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0)...(0)
US-09-144-367-3

Query Match 86.3%; Score 16.4; DB 4; Length 1345;
Best Local Similarity 94.4%; Pred. No. 14;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTGTGTGCATCTTTGC 19
|||||
Db 963 GTGTGTGCATCTTTGC 980

RESULT 4
US-09-566-921-54/c
; Sequence 54, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 54
; LENGTH: 5722
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 331485.3
US-09-566-921-54

Query Match 83.2%; Score 15.8; DB 4; Length 5722;
Best Local Similarity 89.5%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTGTGTGCATCTTTGC 19
|||||
Db 5399 GGTGTGTGCATCTTTGC 5381

RESULT 5
US-09-919-039-174/c
; Sequence 174, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaer, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 174
; LENGTH: 5722
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 113580.4
US-09-919-039-174

Query Match 83.2%; Score 15.8; DB 4; Length 5722;
Best Local Similarity 89.5%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTGTGTGCATCTTTGC 19
|||||
Db 5399 GGTGTGTGCATCTTTGC 5381

RESULT 6
US-09-513-999C-16924
; Sequence 16924, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 16924
; LENGTH: 132
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-16924

Query Match 77.9%; Score 14.8; DB 4; Length 132;
Best Local Similarity 88.9%; Pred. No. 73;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTGTGTGCATCTTTG 18
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Db 55 GGTGTGTGCATCTTATG 72

RESULT 7
US-09-513-999C-16738/c
; Sequence 16738, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.

APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513.999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 16738
LENGTH: 402
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-16738

Query Match 77.9%; Score 14.8; DB 4; Length 402;
Best Local Similarity 88.9%; Pred. No. 86;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTGTGGCATTCTTTC 18
Db 147 GGTGTGGCATTCTTTC 130

RESULT 8
US-08-540-118-2/c
Sequence 2, Application US/08540118
Patent No. 5874526
GENERAL INFORMATION:
APPLICANT: Koelen, Marcue J.M.
ATTORNEY/AGENT: Dehaard, Johannes J.W.
TITLE OF INVENTION: New Toxoplasma gondii antigens
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Akzo No. 5874526e1 Patent Department
STREET: 1300 Piccard Drive, Suite 206
CITY: Rockville
STATE: Maryland
COUNTRY: U.S.A.
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/540.118
FILING DATE: 06-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 942028994
FILING DATE: 06-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gornley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1617 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Toxoplasma gondii
STRAIN: RH
IMMEDIATE SOURCE:
CLONE: #114
US-08-540-118-2

Query Match 77.9%; Score 14.8; DB 2; Length 1617;
Best Local Similarity 88.9%; Pred. No. 1,1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTGTGGCATTCTTTC 19
Db 1385 GTGTGGCATTCTTTC 1368

RESULT 9
US-09-185-818-2/c
Sequence 2, Application US/09185818
Patent No. 6420540
GENERAL INFORMATION:
APPLICANT: Koelen, Marcue J.M.
ATTORNEY/AGENT: Dehaard, Johannes J.W.
TITLE OF INVENTION: New Toxoplasma gondii antigens
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Akzo No. 6420540e1 Patent Department
STREET: 1300 Piccard Drive, Suite 206
CITY: Rockville
STATE: Maryland
COUNTRY: U.S.A.
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/185.818
FILING DATE: 04-NOV-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/540.118
FILING DATE: 06-OCT-1995
APPLICATION NUMBER: EP 942028994
FILING DATE: 06-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gornley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1617 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Toxoplasma gondii
STRAIN: RH
IMMEDIATE SOURCE:
CLONE: #114
US-09-185-818-2

Query Match 77.9%; Score 14.8; DB 4; Length 1617;
Best Local Similarity 88.9%; Pred. No. 1,1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTGTGGCATTCTTTC 19
Db 1385 GTGTGGCATTCTTTC 1368

RESULT 10
US-09-671-317-485
Sequence 485, Application US/09671317
Patent No. 6528260
GENERAL INFORMATION:

APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Bouguerec, Lydie
APPLICANT: Cohen, Amick
TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
FILE REFERENCE: 62.US3.CIP
CURRENT APPLICATION NUMBER: US/09/671,317
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 09/536,178
PRIOR FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: PCT/IB00/00403
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/126,269
PRIOR FILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: US 60/131,961
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 977
SOFTWARE: Patent.pm
SEQ ID NO 485
LENGTH: 49312
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 5466..7466
OTHER INFORMATION: 5'regulatory region
NAME/KEY: exon
LOCATION: 7467..7725
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 20256..20355
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 36905..36975
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 45167..45248
OTHER INFORMATION: exon 4
NAME/KEY: exon
LOCATION: 45728..45965
OTHER INFORMATION: exon 5
NAME/KEY: misc feature
LOCATION: 45966..49312
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 7564
OTHER INFORMATION: 10-286-289 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 7619
OTHER INFORMATION: 10-286-345 : polymorphic base A or T
NAME/KEY: allele
LOCATION: 7649
OTHER INFORMATION: 10-286-375 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 17258
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NAME/KEY: allele
LOCATION: 21590
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NAME/KEY: allele
LOCATION: 21595
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NAME/KEY: allele
LOCATION: 36971
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LOCATION: 45214
OTHER INFORMATION: 10-289-201 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 45741
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NAME/KEY: allele
LOCATION: 46029

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NAME/KEY: allele
LOCATION: 46032
OTHER INFORMATION: 10-290-328 : deletion of G
NAME/KEY: primer bind
LOCATION: 7276..7294
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NAME/KEY: primer bind
LOCATION: 7676..7694
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NAME/KEY: primer bind
LOCATION: 16839..16856
OTHER INFORMATION: 12-425.rp
NAME/KEY: primer bind
LOCATION: 17297..17314
OTHER INFORMATION: 12-425.pu complement
NAME/KEY: primer bind
LOCATION: 21456..21474
OTHER INFORMATION: 12-421.pu
NAME/KEY: primer bind
LOCATION: 21886..21906
OTHER INFORMATION: 12-421.rp complement
NAME/KEY: primer bind
LOCATION: 36740..36758
OTHER INFORMATION: 10-523.pu
NAME/KEY: primer bind
LOCATION: 36997..37015
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LOCATION: 45020..45037
OTHER INFORMATION: 10-289.pu
NAME/KEY: primer bind
LOCATION: 45413..45432
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OTHER INFORMATION: 10-286-289.mis
NAME/KEY: primer bind
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LOCATION: 7600..7618
OTHER INFORMATION: 10-286-345.mis
NAME/KEY: primer bind
LOCATION: 7620..7638
OTHER INFORMATION: 10-286-345.mis complement
NAME/KEY: primer bind
LOCATION: 7630..7648
OTHER INFORMATION: 10-286-375.mis
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LOCATION: 7650..7668
OTHER INFORMATION: 10-286-375.mis complement
NAME/KEY: primer bind
LOCATION: 17239..17257
OTHER INFORMATION: 12-425-57.mis
NAME/KEY: primer bind
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NAME/KEY: primer bind
LOCATION: 21596..21614
OTHER INFORMATION: 12-421-140.mis
NAME/KEY: primer bind
LOCATION: 36952..36970
OTHER INFORMATION: 10-523-232.mis


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LOCATION: 36972..36990
OTHER INFORMATION: 10-523-232.mis complement
NAME/KEY: primer_bind
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OTHER INFORMATION: 10-289-201.mis
NAME/KEY: primer_bind
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NAME/KEY: primer_bind
LOCATION: 45722..45740
OTHER INFORMATION: 10-290-37.mis
NAME/KEY: primer_bind
LOCATION: 45742..45760
OTHER INFORMATION: 10-290-37.mis complement
NAME/KEY: primer_bind
LOCATION: 46010..46028
OTHER INFORMATION: 10-290-326.mis
NAME/KEY: primer_bind
LOCATION: 46030..46048
OTHER INFORMATION: 10-290-326.mis complement
NAME/KEY: misc_binding
LOCATION: 7552..7576
OTHER INFORMATION: 10-286-289.probe
NAME/KEY: misc_binding
LOCATION: 7607..7631
OTHER INFORMATION: 10-286-345.probe
NAME/KEY: misc_binding
LOCATION: 7637..7661
OTHER INFORMATION: 10-286-375.probe
NAME/KEY: misc_binding
LOCATION: 17246..17270
OTHER INFORMATION: 12-425-57.probe
NAME/KEY: misc_binding
LOCATION: 21583..21607
OTHER INFORMATION: 12-421-140.probe
NAME/KEY: misc_binding
LOCATION: 36955..36983
OTHER INFORMATION: 10-523-232.probe
NAME/KEY: misc_binding
LOCATION: 45202..45226
OTHER INFORMATION: 10-289-201.probe
NAME/KEY: misc_binding
LOCATION: 45725..45753
OTHER INFORMATION: 10-280-37.probe
NAME/KEY: misc_binding
LOCATION: 46017..46041
OTHER INFORMATION: 10-290-326.probe
US-09-671-317-485
```

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Query Match 77.8%; Score 14.8; DB 4; Length 49312;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGTGCGATTCCTTGC 19
DB 16640 GTGTGCGATTCCTTGC 16657

RESULT 11
US-09-513-999C-18974
Sequence 18974, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J. B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J. Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513.999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
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PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 18974
LENGTH: 250
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-18974
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Query Match 75.8%; Score 14.4; DB 4; Length 250;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 2 GTGTGCGATTCCTT 17
DB 190 GTGTGCGATTCCTT 205
```

```
RESULT 12
US-09-702-705-1647/c
Sequence 1647, Application US/09702705
Patent No. 6504010
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702.705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: PaateSeq for Windows Version 3.0
SEQ ID NO 1647
LENGTH: 451
TYPE: DNA
ORGANISM: Homo sapiens
US-09-702-705-1647
```

```
Query Match 75.8%; Score 14.4; DB 4; Length 451;
Best Local Similarity 93.8%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 3 TGTGTGCGATTCCTTG 18
DB 379 TGTGTGCGATTCCTTG 364
```

```
RESULT 13
US-09-736-457-1647/c
Sequence 1647, Application US/09736457
Patent No. 6509448
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Pan, Liqun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736.457
```

```
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1647
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-736-457-1647

Query Match
Best Local Similarity 75.8%; Score 14.4; DB 4; Length 451;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGTGTGCGATTCTTTG 18
Db 379 TGTGTGCTATTCTTTG 364

RESULT 14
US-09-614-124B-1647/c
; Sequence 1647, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1647
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-614-124B-1647

Query Match
Best Local Similarity 75.8%; Score 14.4; DB 4; Length 451;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGTGTGCGATTCTTTG 18
Db 379 TGTGTGCTATTCTTTG 364

RESULT 15
US-09-671-325-1647/c
; Sequence 1647, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1647
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-671-325-1647

Query Match
Best Local Similarity 75.8%; Score 14.4; DB 4; Length 451;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGTGTGCGATTCTTTG 18
Db 379 TGTGTGCTATTCTTTG 364

Search completed: January 26, 2005, 13:15:22
Job time : 27.0917 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 13:15:32 ; Search time 134.689 Seconds
(without alignments)
810.549 Million cell updates/sec

Title: US-10-085-612A-21

Perfect score: 19

Sequence: 1 ggcgtgcgcattcttgc 19

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

8600550

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	1254	14	US-10-085-612-4
2	16.4	86.3	1345	14	US-09-943-115A-1
3	16.4	86.3	1345	14	US-10-146-575-3
4	16.4	86.3	1345	14	US-10-085-612-3
5	16.4	86.3	1345	14	US-10-257-166-149
6	16.4	86.3	13035	15	US-10-121-960C-14
7	16.4	86.3	15185	15	US-10-121-960C-17
8	15.8	83.2	225	15	US-10-098-2638-23844
9	15.8	83.2	50	16	US-10-252-287-3
10	15.8	83.2	50	16	US-10-252-287-4
11	15.8	83.2	191	18	US-10-425-115-174784
12	15.8	83.2	322	9	US-09-960-352-11673

13	15.8	83.2	581	13	US-10-027-632-19705	Sequence 19705, A
14	15.8	83.2	581	13	US-10-027-632-19705	Sequence 19705, A
15	15.8	83.2	720	13	US-10-027-632-155127	Sequence 155127, A
16	15.8	83.2	720	13	US-10-027-632-155127	Sequence 155127, A
17	15.8	83.2	2000	9	US-09-938-842A-3958	Sequence 3958, Ap
18	15.8	83.2	2000	11	US-09-938-842A-3958	Sequence 3958, Ap
19	15.8	83.2	5722	10	US-09-919-039-174	Sequence 174, App
20	15.8	83.2	6487	18	US-10-335-053-159	Sequence 159, App
21	15.4	81.1	396	9	US-09-960-352-10415	Sequence 10415, A
22	15.4	81.1	414	9	US-09-960-352-10901	Sequence 10901, A
23	15.4	81.1	493	10	US-09-918-995-17875	Sequence 17875, A
24	14.8	77.9	162	18	US-10-674-124A-9954	Sequence 9954, Ap
25	14.8	77.9	230	18	US-10-425-115-127551	Sequence 127551, A
26	14.8	77.9	294	17	US-10-437-963-17881	Sequence 17881, A
27	14.8	77.9	301	18	US-10-425-115-41613	Sequence 41613, A
28	14.8	77.9	372	10	US-09-803-719-797	Sequence 797, App
29	14.8	77.9	386	18	US-10-674-124A-6241	Sequence 6241, Ap
30	14.8	77.9	388	9	US-09-960-352-10766	Sequence 10766, A
31	14.8	77.9	427	18	US-10-674-124A-6240	Sequence 6240, Ap
32	14.8	77.9	468	13	US-10-027-632-300031	Sequence 300031, A
33	14.8	77.9	468	15	US-10-027-632-300031	Sequence 300031, A
34	14.8	77.9	471	17	US-10-437-963-59066	Sequence 59066, A
35	14.8	77.9	492	16	US-10-276-774-299	Sequence 299, App
36	14.8	77.9	553	13	US-10-027-632-191054	Sequence 191054, A
37	14.8	77.9	553	13	US-10-027-632-191055	Sequence 191055, A
38	14.8	77.9	553	15	US-10-027-632-191054	Sequence 191054, A
39	14.8	77.9	553	15	US-10-027-632-191055	Sequence 191055, A
40	14.8	77.9	559	13	US-10-027-632-222524	Sequence 222524, A
41	14.8	77.9	559	13	US-10-027-632-222525	Sequence 222525, A
42	14.8	77.9	559	13	US-10-027-632-222526	Sequence 222526, A
43	14.8	77.9	559	15	US-10-027-632-222525	Sequence 222525, A
44	14.8	77.9	559	15	US-10-027-632-222526	Sequence 222526, A
45	14.8	77.9	559	15	US-10-027-632-222526	Sequence 222526, A

ALIGNMENTS

RESULT 1

US-10-085-612-4

Sequence 4, Application US/10085612

Publication No. US20030096251A1

GENERAL INFORMATION:

APPLICANT: Guida, Marco

APPLICANT: Hall, Jeff

APPLICANT: Petrov, William

APPLICANT: Vredenburg, James

APPLICANT: Colvin, Oliver

APPLICANT: Marks, Jeffrey

TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals

FILE REFERENCE: 4389-5-Cl

CURRENT APPLICATION NUMBER: US/10/085,612

CURRENT FILING DATE: 2002-02-26

PRIOR APPLICATION NUMBER: 09/144,367

PRIOR FILING DATE: 1998-08-31

PRIOR APPLICATION NUMBER: 60/271,630

PRIOR FILING DATE: 2001-02-26

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 1254

TYPE: DNA

ORGANISM: Homo sapiens

US-10-085-612-4

Query Match 100.0%; Score 19; DB 14; Length 1254;

Best Local Similarity 100.0%; Pred. No. 8.9; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGTGTCGATTCCTTGC 19

Db 996 GGTGTGTCGATTCCTTGC 1014

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RESULT 2
US-09-943-115A-1
; Sequence 1, Application US/09943115A
; Publication No. US20030017469A1
; GENERAL INFORMATION:
; APPLICANT: SEQUENOM, Inc.
; APPLICANT: Risinger, Carl
; APPLICANT: Andersson, Maria
; APPLICANT: Lewander, Tommy
; APPLICANT: Olaisson, Erik
; TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9
; FILE REFERENCE: 52459-20021.00
; CURRENT APPLICATION NUMBER: US/09/943.115A
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: UK 0021286.0
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-943-115A-1
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Query Match      86.3%; Score 16.4; DB 10; Length 1345;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      2 GTGTGTCGATCTTTGC 19
      |||||
Db      963 GTGTGTGATCTTTGC 980
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RESULT 3
US-10-146-575-3
; Sequence 3, Application US/10146575
; Publication No. US20030059800A1
; GENERAL INFORMATION:
; APPLICANT: Lichte, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/10/146.575
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US/09/144.367
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0)...(0)
US-10-146-575-3
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Query Match      86.3%; Score 16.4; DB 14; Length 1345;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 GTGTGTCGATCTTTGC 19
      |||||
Db      963 GTGTGTGATCTTTGC 980
```

```
RESULT 4
US-10-085-612-3
; Sequence 3, Application US/10085612
; Publication No. US20030096251A1
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; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Vredenburg, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Marks, Jeffrey
; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
; FILE REFERENCE: 4389-5-C1
; CURRENT APPLICATION NUMBER: US/10/085.612
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144.367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271.630
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-612-3
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Query Match      86.3%; Score 16.4; DB 14; Length 1345;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 GTGTGTCGATCTTTGC 19
      |||||
Db      963 GTGTGTGATCTTTGC 980
```

```
RESULT 5
US-10-257-166-149
; Sequence 149, Application US/10257166
; Publication No. US20040023230A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation of
; FILE REFERENCE: 5013.1011
; CURRENT APPLICATION NUMBER: US/10/257.166
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: PCT/EP01/07470
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-06-29
; 2000-06-30
; 2000-09-01
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 149
; LENGTH: 8776
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-257-166-149
```

```
Query Match      86.3%; Score 16.4; DB 16; Length 8776;
Best Local Similarity 94.4%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 GGTTGTGCGATCTTTG 18
      |||||
Db      4900 GGTTGTGCGATTTTGG 4917
```

```
RESULT 6
US-10-121-960C-14
; Sequence 14, Application US/10121960C
```

```
; Publication No. US20030145341A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, Weisheng
; APPLICANT: CONTAG, Pamela
; APPLICANT: PURCHIO, Anthony
; APPLICANT: HASHIMA, Sandy
; APPLICANT: MA, Shirley
; APPLICANT: NAMOTKA, Kevin
; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
; TITLE OF INVENTION: TRANSCRIPTION CONTROL ELEMENTS ASSOCIATED WITH
; TITLE OF INVENTION: CYTOCHROME EXPRESSION
; FILE REFERENCE: 9400-0014 / PEX-014.US
; CURRENT APPLICATION NUMBER: US/10/121,960C
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 13035
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human CYP3A4 gene locus
; US-10-121-960C-14

Query Match      86.3%; Score 16.4; DB 15; Length 13035;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GTGTGTGCAGATTCCTTGC 19
Db      12788 GTGTGTGCAGATTCCTTGC 12805

RESULT 7
US-10-121-960C-17
; Sequence 17, Application US/10121960C
; Publication No. US20030145341A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, Weisheng
; APPLICANT: CONTAG, Pamela
; APPLICANT: PURCHIO, Anthony
; APPLICANT: HASHIMA, Sandy
; APPLICANT: MA, Shirley
; APPLICANT: NAMOTKA, Kevin
; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
; TITLE OF INVENTION: TRANSCRIPTION CONTROL ELEMENTS ASSOCIATED WITH
; FILE REFERENCE: 9400-0014 / PEX-014.US
; CURRENT APPLICATION NUMBER: US/10/121,960C
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 15185
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CYP3A4-luc transgene
; US-10-121-960C-17

Query Match      86.3%; Score 16.4; DB 15; Length 15185;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GTGTGTGCAGATTCCTTGC 19
Db      12788 GTGTGTGCAGATTCCTTGC 12805

RESULT 8
US-10-098-263B-23844/c
; Sequence 23844, Application US/10098263B
; Publication No. US20030104410A1
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; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 23844
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-098-263B-23844

Query Match      83.2%; Score 15.8; DB 15; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGTTGTGCAGATTCCTTGC 19
Db      25 GGTTGTGCAGATTCCTTGC 7

RESULT 9
US-10-252-287-3
; Sequence 3, Application US/10252287
; Publication No. US20040059102A1
; GENERAL INFORMATION:
; APPLICANT: Lucent Technologies Inc.
; APPLICANT: Mills, Jr., Allen P
; APPLICANT: Yurke, Bernard
; TITLE OF INVENTION: COMPOSITIONS THAT REVERSIBLY GEL AND DE-GEL
; FILE REFERENCE: MILLS 18-14
; CURRENT APPLICATION NUMBER: US/10/252,287
; CURRENT FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: a oligonucleotide that ser
; OTHER INFORMATION: ves as a cross-linking agent for a polyacrylamide gel
; US-10-252-287-3

Query Match      83.2%; Score 15.8; DB 16; Length 50;
Best Local Similarity 89.5%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGTTGTGCAGATTCCTTGC 19
Db      26 GGTTGTGCAGATTCCTTGC 44

RESULT 10
US-10-252-287-4/c
; Sequence 4, Application US/10252287
; Publication No. US20040059102A1
; GENERAL INFORMATION:
; APPLICANT: Lucent Technologies Inc.
; APPLICANT: Mills, Jr., Allen P
; APPLICANT: Yurke, Bernard
; TITLE OF INVENTION: COMPOSITIONS THAT REVERSIBLY GEL AND DE-GEL
; FILE REFERENCE: MILLS 18-14
; CURRENT APPLICATION NUMBER: US/10/252,287
; CURRENT FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 50
```

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: a oligonucleotide that sex
OTHER INFORMATION: ves as a removal agent for a cross-linked polyacrylamide gel
US-10-252-287-4

Query Match 83.2%; Score 15.8; DB 16; Length 50;
Best Local Similarity 89.5%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGGTGTGCGATTCTTTC 19
DB 25 GGGTGTGCGATTCTTAC 7

RESULT 11
US-10-425-115-174784/C
Sequence 174784, Application US/10425115
Publication No. US2004021472A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 174784
LENGTH: 191
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MFT4577_90986C.1
US-10-425-115-174784

Query Match 83.2%; Score 15.8; DB 18; Length 191;
Best Local Similarity 89.5%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGGTGTGCGATTCTTTC 19
DB 107 GGGTGTGCGATTCTCAGC 89

RESULT 12
US-09-960-352-11673/C
Sequence 11673, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengding
APPLICANT: Byatt, John C.
APPLICANT: Machialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 11673
LENGTH: 322
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 50-LIB3057-019-Q1-K1-E10
US-09-960-352-11673

Query Match 83.2%; Score 15.8; DB 9; Length 322;
Best Local Similarity 89.5%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGGTGTGCGATTCTTTC 19
DB 236 GGGTGTGCGATTCTTTC 218

RESULT 13
US-10-027-632-19705
Sequence 19705, Application US/10027632
Publication No. US2002019837A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19705
LENGTH: 581
TYPE: DNA
ORGANISM: Human
US-10-027-632-19705

Query Match 83.2%; Score 15.8; DB 13; Length 581;
Best Local Similarity 89.5%; Pred. No. 3.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGGTGTGCGATTCTTTC 19
DB 399 GGGTGTGCGATTCTTTC 417

RESULT 14
US-10-027-632-19705
Sequence 19705, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 19705
 LENGTH: 581
 TYPE: DNA
 ORGANISM: Human
 US-10-027-632-19705

Query Match 83.2%; Score 15.8; DB 13; Length 581;
 Best Local Similarity 89.5%; Pred. No. 3.6e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGATGTCGATCTTGC 19
 |||||
 Db 399 GGATGTCGATCTTGC 417

RESULT 15
 US-10-027-632-155127
 ; Sequence 155127, Application US/10027632
 ; Publication No. US20020198371A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; TITLE OF INVENTION: Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 155127
 ; LENGTH: 720
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-10-027-632-155127

Query Match 83.2%; Score 15.8; DB 13; Length 720;
 Best Local Similarity 89.5%; Pred. No. 3.7e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGATGTCGATCTTGC 19
 |||||
 Db 540 GGATGTCGATCTTGC 558

Search completed: January 26, 2005, 18:15:48
 Job time : 135.689 secs

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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 11:30:01 ; Search time 27.333 Seconds
(without alignment)
520.089 Million cell updates/sec

Title: US-10-085-612A-22

Sequence: 1 cccgcacagcagctcttag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA: *
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCtUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfileseq1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17.4	87.0	1230025	4 US-09-198-452A-1	Sequence 1, Appli
2	16.8	84.0	2492	3 US-08-695-191-3	Sequence 3, Appli
3	16.8	84.0	2492	3 US-08-682-080-3	Sequence 3, Appli
4	16.8	84.0	2492	4 US-09-096-648-3	Sequence 3, Appli
5	16.8	84.0	2517	3 US-09-534-407-5	Sequence 5, Appli
6	16.8	84.0	2517	4 US-09-999-201B-2	Sequence 2, Appli
7	16.8	84.0	2517	4 US-10-281-673A-2	Sequence 2, Appli
8	15.8	79.0	1547	4 US-09-800-729-76	Sequence 76, Appli
9	15.4	77.0	65	1 US-08-190-687B-9	Sequence 9, Appli
10	15.4	77.0	3456	1 US-08-190-687B-24	Sequence 24, Appli
11	15.4	77.0	63000	4 US-09-786-172-18	Sequence 18, Appli
12	15.2	76.0	278	4 US-09-313-284A-5792	Sequence 987, App
13	15.2	76.0	286	4 US-09-313-294A-987	Sequence 987, App
14	15.2	76.0	328	4 US-09-023-655-471	Sequence 8, Appli
15	15.2	76.0	630	4 US-09-733-167A-8	Sequence 8, Appli
16	15.2	76.0	1045	3 US-08-859-157-3	Sequence 3, Appli
17	15.2	76.0	1045	3 US-09-109-273-3	Sequence 3, Appli
18	15.2	76.0	1045	3 US-09-276-993-3	Sequence 3, Appli
19	15.2	76.0	1045	4 US-09-723-450-3	Sequence 3, Appli
20	15.2	76.0	1142	4 US-09-733-167A-2	Sequence 2, Appli
21	15.2	76.0	1230	4 US-09-023-669-3	Sequence 3, Appli
22	15.2	76.0	1230	4 US-09-603-567-3	Sequence 3, Appli
23	15.2	76.0	1553	3 US-09-022-669-1	Sequence 1, Appli
24	15.2	76.0	1553	4 US-09-603-567-1	Sequence 1, Appli
25	15.2	76.0	1737	3 US-09-173-151A-1	Sequence 1, Appli
26	15.2	76.0	2061	3 US-09-173-151A-3	Sequence 3, Appli
27	15.2	76.0	16595	3 US-09-146-053-7	Sequence 7, Appli

28	15.2	76.0	48974	3 US-08-920-422-17	Sequence 17, Appli
29	15	75.0	544	4 US-09-370-838-280	Sequence 280, App
30	15	75.0	544	4 US-09-854-133-280	Sequence 280, App
31	15	75.0	5917	3 US-08-692-922-1	Sequence 1, Appli
32	15	75.0	54945	4 US-09-967-669-10	Sequence 10, Appli
33	14.8	74.0	71	1 US-08-400-440A-83	Sequence 83, Appli
34	14.8	74.0	71	1 US-08-463-093A-83	Sequence 83, Appli
35	14.8	74.0	71	2 US-08-460-888A-83	Sequence 83, Appli
36	14.8	74.0	71	2 US-08-894-578-83	Sequence 83, Appli
37	14.8	74.0	71	3 US-09-412-017-83	Sequence 83, Appli
38	14.8	74.0	322	4 US-09-513-999C-16959	Sequence 16959, A
39	14.8	74.0	426	4 US-09-513-999C-10945	Sequence 10945, A
40	14.8	74.0	495	4 US-09-620-312D-689	Sequence 689, App
41	14.8	74.0	510	4 US-09-621-976-18004	Sequence 18004, A
42	14.8	74.0	637	4 US-09-602-787A-107	Sequence 107, App
43	14.8	74.0	1001	4 US-09-641-638-440	Sequence 440, App
44	14.8	74.0	1001	4 US-10-170-097-440	Sequence 440, App
45	14.8	74.0	1140	1 US-08-348-792-11	Sequence 11, Appli

ALIGNMENTS

RESULT 1
US-09-198-452A-1/c
Sequence 1, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Grifflais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevent
FILE REFERENCE: 9710-003-999
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1
LENGTH: 1230025
TYPER: DNA
ORGANISM: Chlamydia pneumoniae
FEATURE:
NAME/KEY: misc feature
LOCATION: (1) ..(15000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (15001) ..(30000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (30001) ..(45000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (45001) ..(60000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (60001) ..(75000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (75001) ..(90000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (90001) ..(105000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (105001) ..(120000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (120001) ..(135000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (135001) ..(150000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (150001) ..(165000)

LOCATION: (885001)..(900000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (900001)..(915000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature

Query Match 87.0%; Score 17.4; DB 4; Length 1230025;
Best Local Similarity 94.7%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCTGCACAGCAGCTCTTAGG 20
Db 691511 CCTGCACAGCAGCTCTTAGG 691493

RESULT 2

US-08-695-191-3
; Sequence 3, Application US/08695191
; Patent No. 6025155
; GENERAL INFORMATION:
; APPLICANT: Hadlaczky, Gyula
; APPLICANT: Szalay, Aladar
; TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND
; TITLE OF INVENTION: METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FaastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,191
; FILING DATE: 07-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 15-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/629,822
; FILING DATE: 10-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6869-402C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2492 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; US-08-695-191-3

Query Match 84.0%; Score 16.8; DB 3; Length 2492;

Best Local Similarity 90.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCTGCACAGCAGCTCTTAGG 20
Db 2082 CCTGCACAGCAGCTCTTAGG 2101

RESULT 3

US-08-682-080-3
; Sequence 3, Application US/08682080
; Patent No. 6077697
; GENERAL INFORMATION:
; APPLICANT: Hadlaczky, Gyula
; APPLICANT: Szalay, Aladar
; TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND METHODS FOR
; TITLE OF INVENTION: PREPARING ARTIFICIAL CHROMOSOMES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FaastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,080
; FILING DATE: 10-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/629,822
; FILING DATE: 10-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6869-402B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2492 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; US-08-682-080-3

Query Match 84.0%; Score 16.8; DB 3; Length 2492;
Best Local Similarity 90.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCTGCACAGCAGCTCTTAGG 20
Db 2082 CCTGCACAGCAGCTCTTAGG 2101

RESULT 4

US-09-096-648-3
; Sequence 3, Application US/09096648
; Patent No. 6743967

```

; GENERAL INFORMATION:
; APPLICANT: Hadlaczky, Gyula
; APPLICANT: Szalay, Aladar
; TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND
; TITLE OF INVENTION: METHODS PREPARING ARTIFICIAL CHROMOSOMES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,648
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/629,822
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6869-402A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2492 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: Genomic DNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; US-09-096-648-3

Query Match      84.0%; Score 16.8; DB 4; Length 2492;
Best Local Similarity 90.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  CCTGCACAGCAGCTTAGG 20
        |||||
Db      2082 CCTGCACAGCAGCTTAGG 2101

RESULT 5
US-09-534-407-5
; Sequence 5, Application US/09534407
; Patent No. 6361973
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Kimberly Brown
; TITLE OF INVENTION: Promoters For Expressing Genes In A
; TITLE OF INVENTION: Fungal Cell
; FILE REFERENCE: 5611.200-US
; CURRENT APPLICATION NUMBER: US/09/534,407
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/274,449
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 5
; LENGTH: 2517
; TYPE: DNA
; ORGANISM: Fusarium
; US-09-534-407-5

Query Match      84.0%; Score 16.8; DB 3; Length 2517;
Best Local Similarity 90.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  CCTGCACAGCAGCTTAGG 20
        |||||
Db      1016 CCTGCTCAGCAGCTCAGG 1035

RESULT 6
US-09-999-201B-2
; Sequence 2, Application US/09999201B
; Patent No. 6518044
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy
; APPLICANT: Rey, Michael
; APPLICANT: Brown, Kimberly
; TITLE OF INVENTION: Promoters For Expressing Genes In A
; TITLE OF INVENTION: Fungal Cell
; FILE REFERENCE: 5611.210-US
; CURRENT APPLICATION NUMBER: US/09/999,201B
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 09/534,407
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/274,449
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2517
; TYPE: DNA
; ORGANISM: Fusarium
; US-09-999-201B-2

Query Match      84.0%; Score 16.8; DB 4; Length 2517;
Best Local Similarity 90.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  CCTGCACAGCAGCTTAGG 20
        |||||
Db      1016 CCTGCTCAGCAGCTCAGG 1035

RESULT 7
US-10-281-673A-2
; Sequence 2, Application US/10281673A
; Patent No. 6692940
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy
; APPLICANT: Rey, Michael
; APPLICANT: Brown, Kimberly
; TITLE OF INVENTION: Promoters For Expressing Genes In A
; TITLE OF INVENTION: Fungal Cell
; FILE REFERENCE: 5611.220-US
; CURRENT APPLICATION NUMBER: US/10/281,673A
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/534,407
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/274,449
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2517
; TYPE: DNA
; ORGANISM: Fusarium
; US-10-281-673A-2
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Query Match 84.0%; Score 16.8; DB 4; Length 2517;
Best Local Similarity 90.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGCACAGCAGTCTTAGG 20
DB 1016 CCTGCTCAGCAGTCTGAGG 1035

RESULT 8
US-09-800-729-76
Sequence 76, Application US/09800729
Patent No. 6605592
GENERAL INFORMATION:

APPLICANT: NI et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 76
LENGTH: 1547
TYPE: DNA
ORGANISM: Homo sapiens
US-09-800-729-76

Query Match 79.0%; Score 15.8; DB 4; Length 1547;
Best Local Similarity 89.5%; Pred. No. 73;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTGCACAGCAGTCTTAGG 20
DB 498 CCTGCACAGCAGTCTGAGG 516

RESULT 9
US-08-190-687B-9/C
Sequence 9, Application US/08190687B
Patent No. 5760203
GENERAL INFORMATION:
APPLICANT: Wong, Gail L.
APPLICANT: Martin, George
APPLICANT: McCormick, Francis P.
APPLICANT: Rubinfeld, Bonnie
APPLICANT: O'Rourke, Edward C.
APPLICANT: Clark, Robin
TITLE OF INVENTION: GAP Gene Sequences
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,687B
FILING DATE: 02-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/774,644
FILING DATE: 11-OCT-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/260,807
FILING DATE: 21-OCT-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/230,761
FILING DATE: 10-AUG-1988
ATTORNEY/AGENT INFORMATION:
NAME: Gase, David A.
REGISTRATION NUMBER: 27527/31898
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 65 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-190-687B-9

Query Match 77.0%; Score 15.4; DB 1; Length 65;
Best Local Similarity 94.1%; Pred. No. 75;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCTGCACAGCAGTCTTA 18
DB 23 CCTGAACAGCAGTCTTA 7

RESULT 10
US-08-190-687B-24/C
Sequence 24, Application US/08190687B
Patent No. 5760203
GENERAL INFORMATION:
APPLICANT: Wong, Gail L.
APPLICANT: Martin, George
APPLICANT: McCormick, Francis P.
APPLICANT: Rubinfeld, Bonnie
APPLICANT: O'Rourke, Edward C.
APPLICANT: Clark, Robin
TITLE OF INVENTION: GAP Gene Sequences
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,687B
FILING DATE: 02-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/774,644
FILING DATE: 11-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/260,807
FILING DATE: 21-OCT-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/230,761
FILING DATE: 10-AUG-1988
ATTORNEY/AGENT INFORMATION:
NAME: Gase, David A.
REGISTRATION NUMBER: 38,153

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REFERENCE/DOCKET NUMBER: 27527/31898
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 3456 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 100..2709
US-08-190-687B-24

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 3456;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CCTGCACAGCAGTCTTA 18
Db 65 CCTGCACAGCAGTCTTA 49

RESULT 11
US-09-780-172-18/c
Sequence 18, Application US/09780172
Patent No. 6607916
GENERAL INFORMATION:
APPLICANT: Robert McKay
APPLICANT: Susan M. Preler
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA EXPRESSION
FILE REFERENCE: RRS-0159
CURRENT APPLICATION NUMBER: US/09/780,172
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 18
LENGTH: 63000
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-780-172-18

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 4; Length 63000;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CCTGCACAGCAGTCTTA 18
Db 56617 CCTGCACAGCAGTCTTA 56601

RESULT 12
US-09-313-294A-5792/c
Sequence 5792, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Laligudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 5792
LENGTH: 278
TYPE: DNA
ORGANISM: Zea mays
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FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700350690H1
NAME/KEY: unsure
LOCATION: 14, 17, 22-23, 55, 85, 151, 159, 181, 185, 202, 212, 229, 240, 245, 251,
OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-5792

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 4; Length 278;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCTGCACAGCAGTCTTAGG 20
Db 49 CGCTGCACGCGCAGTTTAGG 30

RESULT 13
US-09-313-294A-987/c
Sequence 987, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Laligudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 987
LENGTH: 286
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700550186H1
US-09-313-294A-987

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 4; Length 286;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCTGCACAGCAGTCTTAGG 20
Db 73 CGCTGCACGCGCAGTTTAGG 54

RESULT 14
US-09-023-655-471/c
Sequence 471, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 471:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: COLNOT08
CLONE: 1844277
US-09-023-655-471

Query Match 76.0%; Score 15.2; DB 4; Length 328;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCTGCACAGCAGTCTTAGG 20
|||
Db 116 CACTGCACAGCAGTCTGCGG 97

RESULT 15
US-09-733-167A-8/C
Sequence 8, Application US/09733167A
Patent No. 6696547
GENERAL INFORMATION:
APPLICANT: Peter, Marcus
TITLE OF INVENTION: Protein for Regulation of Apoptosis
FILE REFERENCE: 4121-120
CURRENT APPLICATION NUMBER: US/09/733,167A
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: PCT/DE99/01712
PRIOR FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: German Patent Application No. 6696547 198 25 621.3
PRIOR FILING DATE: 1998-06-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent version 3.1
SEQ ID NO 8
LENGTH: 630
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Truncated segment of the DNA sequence encoding human DEDD, compri
OTHER INFORMATION: sing nucleotides 352-981 of SEQ ID NO 2.
US-09-733-167A-8

Query Match 76.0%; Score 15.2; DB 4; Length 630;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCTGCACAGCAGTCTTAGG 20
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Db 311 CCTGCACAGCAGTCTCATG 292

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 13:15:32 ; Search time 141.778 Seconds
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Title: US-10-085-612A-22
Perfect score: 20
Sequence: 1 cccgcacagcagctttagg 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqe, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	100.0	1254	14 US-10-085-612-4	Sequence 4, Appl
C 2	17.4	87.0	312	9 US-09-841-132-466	Sequence 466, App
C 3	17.4	87.0	312	18 US-10-872-155-466	Sequence 466, App
C 4	17.4	87.0	617	13 US-10-027-632-259078	Sequence 259078,
C 5	17.4	87.0	617	15 US-10-027-632-259078	Sequence 259078,
C 6	17.4	87.0	1230025	16 US-10-289-762-1	Sequence 1, Appl
C 7	16.8	84.0	201	18 US-10-719-993-18096	Sequence 18096, A
C 8	16.8	84.0	201	18 US-10-719-993-47222	Sequence 47222, A
C 9	16.8	84.0	285	18 US-10-425-115-25647	Sequence 25647, A
C 10	16.8	84.0	488	9 US-09-864-761-11190	Sequence 11190, A
C 11	16.8	84.0	977	18 US-10-653-047-1353	Sequence 1353, Ap
C 12	16.8	84.0	1156	13 US-10-027-632-119142	Sequence 119142,

13	16.8	84.0	1156	15 US-10-027-632-119142	Sequence 119142,
14	16.8	84.0	2111	10 US-09-854-867-145	Sequence 145, App
15	16.8	84.0	2487	14 US-10-082-830-67	Sequence 67, Appl
16	16.8	84.0	2492	9 US-09-096-648-3	Sequence 3, Appl
17	16.8	84.0	2492	9 US-09-799-462A-3	Sequence 3, Appl
18	16.8	84.0	2492	10 US-09-836-911A-3	Sequence 3, Appl
19	16.8	84.0	2492	13 US-10-125-767-3	Sequence 3, Appl
20	16.8	84.0	2492	14 US-10-151-081-3	Sequence 3, Appl
21	16.8	84.0	2492	15 US-10-287-113-3	Sequence 3, Appl
22	16.8	84.0	2492	15 US-10-219-694-3	Sequence 3, Appl
23	16.8	84.0	2492	17 US-10-782-129-3	Sequence 3, Appl
24	16.8	84.0	2492	17 US-10-808-689-3	Sequence 3, Appl
25	16.8	84.0	2517	15 US-10-281-673-5	Sequence 5, Appl
26	16.8	84.0	52312	17 US-10-322-281-753	Sequence 753, App
27	16.8	84.0	152165	18 US-10-719-993-6942	Sequence 6942, Ap
C 28	16.8	84.0	1980090	18 US-10-719-993-6815	Sequence 6815, Ap
C 29	16.4	82.0	696	18 US-10-653-047-7191	Sequence 7191, Ap
C 30	16.4	82.0	1089	9 US-09-841-132-467	Sequence 467, App
C 31	16.4	82.0	1089	18 US-10-872-155-467	Sequence 467, App
C 32	16	80.0	403035	17 US-10-741-601-5729	Sequence 5729, Ap
C 33	15.8	79.0	91	9 US-09-864-761-25055	Sequence 25055, A
C 34	15.8	79.0	201	18 US-10-719-993-24938	Sequence 24938, A
C 35	15.8	79.0	241	15 US-10-029-386-22007	Sequence 22007, A
C 36	15.8	79.0	262	9 US-09-864-761-27307	Sequence 27307, A
C 37	15.8	79.0	457	9 US-09-864-761-10658	Sequence 10658, A
C 38	15.8	79.0	498	13 US-10-027-632-133950	Sequence 133950,
C 39	15.8	79.0	498	15 US-10-027-632-133950	Sequence 133950,
C 40	15.8	79.0	517	10 US-09-770-961-89	Sequence 89, Appl
C 41	15.8	79.0	519	9 US-09-864-761-8324	Sequence 8324, Ap
C 42	15.8	79.0	562	13 US-10-027-632-286546	Sequence 286546,
C 43	15.8	79.0	562	15 US-10-027-632-286546	Sequence 286546,
C 44	15.8	79.0	565	15 US-10-029-386-8307	Sequence 8307, Ap
C 45	15.8	79.0	660	13 US-10-027-632-135364	Sequence 135364,

ALIGNMENTS

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RESULT 1
US-10-085-612-4/C
; Sequence 4, Application US/10085612
; Publication No. US20030096251A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Vredenburg, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Marks, Jeffrey
; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
; FILE REFERENCE: 4389-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1254
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-612-4
Query Match 100.0%; Score 20; DB 14; Length 1254;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 20; Conservative 0; Mismatches 0; Gaps 0;
C 1 1 CCCTGCACAGCAGCTTTAGG 20
Db 1094 CCCTGCACAGCAGCTTTAGG 1075
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RESULT 2
US-09-841-132-466/c
; Sequence 466, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS OF CHLAMYDIAL INFECTION
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841.132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 466
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-841-132-466

Query Match 87.0%; Score 17.4; DB 9; Length 312;
Best Local Similarity 94.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CCTGCACAGCAGCTTAGG 20
Db 253 CCTGCAAGCAGCTTAGG 235

RESULT 3
US-10-872-155-466/c
; Sequence 466, Application US/10872155
; Publication No. US20040234536A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C10
; CURRENT APPLICATION NUMBER: US/10/872.155
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 09/620,412
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 09/598,419
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 09/556,877
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 09/454,684
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/426,571
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 09/410,568
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 09/288,594
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: 09/208,277
; PRIOR FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 466
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-872-155-466

Query Match 87.0%; Score 17.4; DB 18; Length 312;
Best Local Similarity 94.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CCTGCACAGCAGCTTAGG 20
Db 253 CCTGCAAGCAGCTTAGG 235

RESULT 4
US-10-027-632-259078/c
; Sequence 259078, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259078
; LENGTH: 617
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-259078

Query Match 87.0%; Score 17.4; DB 13; Length 617;
Best Local Similarity 94.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCTGCACAGCAGCTTAGG 19
Db 239 CCTGCACAGCAATCTTAG 221

RESULT 5
US-10-027-632-259078/c
; Sequence 259078, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720

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SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259078
; LENGTH: 617
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-259078

Query Match      87.0%; Score 17.4; DB 15; Length 617;
Best Local Similarity 94.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCCTGCACAGCAGCTCTTAG 19
        |||||
Db      239 CCCTGCACAGCAATCTTAG 221

RESULT 6
US-10-289-762-1/c
; Sequence 1, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffls, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(15000)
; OTHER INFORMATION: n=a or c or g or t
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; LOCATION: (15001)..(30000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (30001)..(45000)
; OTHER INFORMATION: n=a or c or g or t
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; LOCATION: (45001)..(60000)
; OTHER INFORMATION: n=a or c or g or t
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; LOCATION: (60001)..(75000)
; OTHER INFORMATION: n=a or c or g or t
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; NAME/KEY: misc_feature
; LOCATION: (75001)..(90000)
; OTHER INFORMATION: n=a or c or g or t
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; LOCATION: (90001)..(105000)
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; OTHER INFORMATION: n=a or c or g or t
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; LOCATION: (270001)..(285000)
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; LOCATION: (285001)..(300000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (300001)..(315000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (315001)..(330000)
; OTHER INFORMATION: n=a or c or g or t
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; NAME/KEY: misc_feature
; LOCATION: (330001)..(345000)
; OTHER INFORMATION: n=a or c or g or t
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; NAME/KEY: misc_feature
; LOCATION: (375001)..(390000)
; OTHER INFORMATION: n=a or c or g or t
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; NAME/KEY: misc_feature
; LOCATION: (390001)..(405000)
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LOCATION: (42001)..(435000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (43501)..(450000)
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NAME/KEY: misc_feature
LOCATION: (45001)..(465000)
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NAME/KEY: misc_feature
LOCATION: (46501)..(480000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (48001)..(495000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (49501)..(510000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (51001)..(525000)
OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc_feature
LOCATION: (52501)..(540000)
OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (60001)..(615000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (61501)..(630000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (63001)..(645000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (64501)..(660000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (66001)..(675000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (67501)..(690000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
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Query Match 87.0%; Score 17.4; DB 16; Length 1230025;
Best Local Similarity 94.7%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 CCTGCACAGCAGCTTTAGG 20
Db 691511 CCTGCACAGCAGCTTTAGG 691493
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RESULT 7
US-10-719-993-18096/c
Sequence 18096, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: CU001496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 5342
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18096
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-10-719-993-18096
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Query Match 84.0%; Score 16.8; DB 18; Length 201;
Best Local Similarity 90.0%; Pred. No. 79;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 CCTGCACAGCAGCTTTAGG 20
Db 126 CCTGCACAGCAGCTTTAGG 107
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RESULT 8
US-10-719-993-47222
Sequence 47222, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: CU001496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 5342
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 47222
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-10-719-993-47222
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Query Match 84.0%; Score 16.8; DB 18; Length 201;
Best Local Similarity 90.0%; Pred. No. 79;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 CCTGCACAGCAGCTTTAGG 20
Db 76 CCTGCACAGCAGCTTTAGG 95
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RESULT 9
US-10-425-115-25647
Sequence 25647, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
```

APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 25647
LENGTH: 285
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_1233C.1
US-10-425-115-25647

Query Match 84.0%; Score 16.8; DB 18; Length 285;
Best Local Similarity 90.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGCACAGCAGCTTTAGG 20
DB 222 CCATGCACAGCAGCTTTATG 241

RESULT 10
US-09-864-761-11190
Sequence 11190, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecomica-X-1
CURRENT FILING DATE: 2001-05-23
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 11190
LENGTH: 488
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005879.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.82
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 0.88
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.68
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.62
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.72
US-09-864-761-11190

Query Match 84.0%; Score 16.8; DB 9; Length 488;
Best Local Similarity 90.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGCACAGCAGCTTTAGG 20
DB 242 CCTGCACAGCAGCCTTAGG 261

RESULT 11
US-10-653-047-1353
Sequence 1353, Application US/10653047
Publication No. US20040229367A1
GENERAL INFORMATION:
APPLICANT: Randy M. Berka
APPLICANT: Jeffrey R. Shuster
APPLICANT: Sakari Kauppinen
APPLICANT: Ib Groth Clausen
APPLICANT: Peter Bjarke Olsen
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 5849.200-US
CURRENT APPLICATION NUMBER: US/10/653,047
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US/09/533,559
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/273,623
PRIOR FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1353
LENGTH: 977
TYPE: DNA
ORGANISM: Fusarium venenatum
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1) ... (977)
OTHER INFORMATION: n = A, T, C or G
US-10-653-047-1353

Query Match 84.0%; Score 16.8; DB 18; Length 977;
Best Local Similarity 90.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGCACAGCAGCTTTAGG 20
DB 192 CCTGCACAGCAGCTCAGG 211

RESULT 12
US-10-027-632-119142
Sequence 119142, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.

```
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119142
; LENGTH: 1156
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-119142
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Query Match      84.0%; Score 16.8; DB 13; Length 1156;
Best Local Similarity 90.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      1 CCTGCACAGCAGCTTTAGG 20
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Db      693 CCTGCACAGCAGCTTTGG 712
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RESULT 13
US-10-027-632-119142
; Sequence 119142, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119142
; LENGTH: 1156
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-119142
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Query Match      84.0%; Score 16.8; DB 15; Length 1156;
Best Local Similarity 90.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      1 CCTGCACAGCAGCTTTAGG 20
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Db      693 CCTGCACAGCAGCTTTGG 712

RESULT 14
US-09-854-867-145
; Sequence 145, Application US/09854867
; Publication No. US20030224356A1
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOEL, H
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/09/854,867
; CURRENT FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145
; LENGTH: 2111
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: (1)..(2111)
; OTHER INFORMATION: ta11
US-09-854-867-145
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Query Match      84.0%; Score 16.8; DB 10; Length 2111;
Best Local Similarity 90.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      1 CCTGCACAGCAGCTTTAGG 20
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Db      133 CCTGCACAGCAGCTTTAGG 152
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RESULT 15
US-10-082-830-67
; Sequence 67, Application US/10082830
; Publication No. US20030077604A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming
; APPLICANT: Recipon, Hevye
; APPLICANT: Salceda, Susana
; APPLICANT: Liu, Chenghua
; APPLICANT: Turner, Leah
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
; FILE REFERENCE: DEX-0249
; CURRENT APPLICATION NUMBER: US/10/082,830
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,802
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 282
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 2487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-082-830-67
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Query Match      84.0%; Score 16.8; DB 14; Length 2487;
Best Local Similarity 90.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      1 CCTGCACAGCAGCTTTAGG 20
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Db      977 CCTGCACAGCAGCTTTAGG 996
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Search completed: January 26, 2005, 18:15:51
Job time : 144.778 secs
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 11:30:01 ; Search time 30.0667 Seconds
(without alignments)
520.089 Million cell updates/sec

Title: US-10-085-612A-23

Perfect score: 22

Sequence: 1 ctgcagcccccacccctccctccc 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfilest.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.8	80.9	452	US-09-322-357-47	Sequence 47, Appl
2	17.8	80.9	867	US-09-270-767-12497	Sequence 12497, A
3	17.4	79.1	795	US-09-795-926-47	Sequence 47, Appl
4	17.4	79.1	1505	US-07-915-246-1	Sequence 1, Appl
5	17.4	79.1	4638	US-09-023-655-1215	Sequence 1215, Ap
6	17.2	78.2	284	US-09-313-294A-6532	Sequence 6532, Ap
7	17.2	78.2	309	US-08-209-747-3	Sequence 3, Appl
8	17.2	78.2	309	US-08-458-298-3	Sequence 3, Appl
9	17.2	78.2	451	US-09-702-705-1647	Sequence 1647, Ap
10	17.2	78.2	451	US-09-736-457-1647	Sequence 1647, Ap
11	17.2	78.2	451	US-09-614-124B-1647	Sequence 1647, Ap
12	17.2	78.2	451	US-09-671-325-1647	Sequence 1647, Ap
13	17.2	78.2	451	US-09-658-824-1647	Sequence 1647, Ap
14	17.2	78.2	492	US-09-621-976-1517	Sequence 1516, Ap
15	17.2	78.2	543	US-09-621-976-1516	Sequence 1516, Ap
16	17.2	78.2	557	US-10-101-464A-168	Sequence 168, App
17	17.2	78.2	1129	US-09-387-699-1	Sequence 1, Appl
18	17.2	78.2	1129	US-09-641-259B-1	Sequence 1, Appl
19	17.2	78.2	1200	US-09-598-401C-36	Sequence 36, Appl
20	17.2	78.2	1407	US-08-688-988-7	Sequence 7, Appl
21	17.2	78.2	2793	US-07-646-537B-1	Sequence 1, Appl
22	17.2	78.2	2932	US-08-999-774A-5	Sequence 5, Appl
23	17.2	78.2	2932	US-09-149-476-165	Sequence 165, App
24	17.2	78.2	2995	US-09-244-805-26	Sequence 26, Appl
25	17.2	78.2	3028	US-09-392-714-2	Sequence 2, Appl
26	17.2	78.2	3246	US-09-270-767-13706	Sequence 13706, A
27	17.2	78.2	3276	US-09-149-476-298	Sequence 298, App

C 28	17.2	78.2	3768	4	US-09-566-921-50	Sequence 50, Appl
C 29	17.2	78.2	3812	4	US-09-784-316-1	Sequence 1, Appl
C 30	17.2	78.2	3812	4	US-10-229-124-1	Sequence 1, Appl
C 31	17.2	78.2	6775	4	US-09-620-312D-289	Sequence 289, App
C 32	17.2	78.2	7672	4	US-09-220-132-24	Sequence 24, Appl
C 33	17.2	78.2	8091	4	US-09-230-652-1	Sequence 1, Appl
C 34	17.2	78.2	8257	4	US-09-484-970B-65	Sequence 65, Appl
C 35	17.2	78.2	19025	4	US-09-849-334-3	Sequence 3, Appl
C 36	17.2	78.2	19025	4	US-10-274-878-3	Sequence 3, Appl
C 37	17.2	78.2	65042	4	US-09-784-316-3	Sequence 3, Appl
C 38	17.2	78.2	65042	4	US-10-229-124-3	Sequence 3, Appl
C 39	17	77.3	206	4	US-09-621-976-9654	Sequence 9654, Ap
C 40	17	77.3	311	4	US-09-621-976-11167	Sequence 11167, A
C 41	17	77.3	447	4	US-09-621-976-14007	Sequence 14007, A
C 42	17	77.3	458	4	US-09-621-976-12510	Sequence 12510, A
C 43	17	77.3	477	4	US-09-621-976-12572	Sequence 12572, A
C 44	17	77.3	480	4	US-09-621-976-10666	Sequence 10666, A
C 45	17	77.3	481	4	US-09-621-976-10533	Sequence 10533, A

ALIGNMENTS

RESULT 1
US-09-322-357-47
Sequence 47, Application US/09322357

Patent No. 6593104

GENERAL INFORMATION:

APPLICANT: STONE, EDWIN M.

FILE REFERENCE: SHEFFIELD, VAL C.

FILE REFERENCE: UUA-018.03

CURRENT APPLICATION NUMBER: US/09/322,357

CURRENT FILING DATE: 1999-05-28

NUMBER OF SEQ ID NOS: 74

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 47

LENGTH: 452

TYPE: DNA

ORGANISM: Homo sapiens

US-09-322-357-47

Query Match
Best Local Similarity 90.5%; Score 17.8; DB 4; Length 452;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGCAGCCCACTCTCTCC 22
Db 45 TGCAGCCCACTCTCTCC 65

RESULT 2

US-09-270-767-12497/c

Sequence 12497, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

FILE REFERENCE: Nucleic acids and proteins of Drosophila melanogaster

CURRENT APPLICATION NUMBER: 7326-094

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 12497

LENGTH: 867

TYPE: DNA

ORGANISM: Drosophila melanogaster

US-09-270-767-12497

Query Match
Best Local Similarity 90.5%; Score 17.8; DB 4; Length 867;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCAGCCCACTCTCTCC 22
Db 463 TGCAGCCCACTCTCTCC 443

RESULT 3

US-09-795-926-47/c
Sequence 47, Application US/09795926
Patent No. 6555669
GENERAL INFORMATION:
APPLICANT: Donoho, Gregory
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Abuin, Alejandro
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
APPLICANT: Walke, D. Wade
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Hu, Yi
APPLICANT: Kieke, James Alvin
APPLICANT: Potter, David George
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE PROTEINS AND
FILE REFERENCE: LEX-0144-USA
CURRENT APPLICATION NUMBER: US/09/795,926
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 60/185,920
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: US 60/186,558
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/191,849
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PastSeq for Windows Version 4.0
SEQ ID NO 47
LENGTH: 795
TYPE: DNA
ORGANISM: homo sapiens
US-09-795-926-47

Query March 79.1%; Score 17.4; DB 4; Length 795;
Best Local Similarity 94.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCCCACTCTCTCC 22
Db 123 CAGCCCACTCTCTCC 105

RESULT 4

US-07-915-246-1/c
Sequence 1, Application US/07915246
Patent No. 5401836
GENERAL INFORMATION:
APPLICANT: Baszczynski, Chris L.
APPLICANT: Fallis, Lynne
APPLICANT: Bellmare, Guy
APPLICANT: Boivin, Rodolphe
TITLE OF INVENTION: A BRASSICA REGULATORY SEQUENCE FOR
TITLE OF INVENTION: ROOT-SPECIFIC OR ROOT-ABUNDANT GENE EXPRESSION
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held, and Malloy
STREET: 500 W. Madison St. 34th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/915,246
FILING DATE: 19920716
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pochopien, Donald J.
REGISTRATION NUMBER: 32,167
REFERENCE/DOCKET NUMBER: 91 P 1125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 707-8869
TELEFAX: 312 707-9155
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1505 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Brassica napus
STRAIN: Westar
DEVELOPMENTAL STAGE: Somatic
TISSUE TYPE: Root
US-07-915-246-1

Query March 79.1%; Score 17.4; DB 1; Length 1505;
Best Local Similarity 94.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCCCACTCTCTCC 22
Db 756 CAGCCCACTCTCTCC 738

RESULT 5

US-09-023-655-1215/c
Sequence 1215, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1215:
SEQUENCE CHARACTERISTICS:
LENGTH: 4638 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g219928
US-09-023-655-1215

Query Match 79.1%; Score 17.4; DB 4; Length 4638;
Best Local Similarity 94.7%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCCCACTCTCTCC 22
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Db 3344 CAGCCCACTCTCTCC 3326

RESULT 6
US-09-313-294A-6532/c
Sequence 6532, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalagudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 6532
LENGTH: 284
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700351966H1
US-09-313-294A-6532

Query Match 78.2%; Score 17.2; DB 4; Length 284;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCAGCCCACTCTCTCC 22
|||||
Db 224 CTGCAGCCCACTCTCTCC 203

RESULT 7
US-08-209-747-3/c
Sequence 3, Application US/08209747
Patent No. 5733771
GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Colgin, Mark
TITLE OF INVENTION: CDNA Encoding Minor Ampullate Spider
TITLE OF INVENTION: Silk Proteins
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolaasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-3487
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/209,747
FILING DATE: 14-MAR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-104P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8050
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: N. clavipes
TISSUE TYPE: minor ampullate gland
FEATURE:
NAME/KEY: CDS
LOCATION: 1..309
OTHER INFORMATION: /product= "amino terminus of MISP2
OTHER INFORMATION: protein"
US-08-209-747-3

Query Match 78.2%; Score 17.2; DB 1; Length 309;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCAGCCCACTCTCTCC 22
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Db 307 CTGCAGCCCACTCTCTCC 286

RESULT 8
US-08-458-298-3/c
Sequence 3, Application US/08458298
Patent No. 5756677
GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Colgin, Mark
TITLE OF INVENTION: CDNA Encoding Minor Ampullate Spider
TITLE OF INVENTION: Silk Proteins
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolaasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-3487
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,298
FILING DATE: 02-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,747
FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977

```
REFERENCE/DOCKET NUMBER: 1447-104P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: N. clavipes
TISSUE TYPE: minor ampullate gland
FEATURE:
NAME/KEY: CDS
LOCATION: 1..309
OTHER INFORMATION: /product= "amino terminus of MISP2
US-08-458-298-3
OTHER INFORMATION: protein"
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Query Match 78.2%; Score 17.2; DB 1; Length 309;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 CTGCAGCCGCCACCTCTTCTCC 22
Db 307 CTGCAGCCGCCACCTCTTCTCC 286
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```
RESULT 9
US-09-702-705-1647
Sequence 1647, Application US/09702705
Patent No. 6504010
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fangier, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darriack
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1647
LENGTH: 451
TYPE: DNA
ORGANISM: Homo sapiens
US-09-702-705-1647
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Query Match 78.2%; Score 17.2; DB 4; Length 451;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 CTGCAGCCGCCACCTCTTCTCC 22
Db 301 CAGCAGCCGCCACCATCTTCC 322
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RESULT 10
US-09-736-457-1647
Sequence 1647, Application US/09736457
Patent No. 6509448
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
```

```
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fangier, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darriack
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1647
LENGTH: 451
TYPE: DNA
ORGANISM: Homo sapiens
US-09-736-457-1647
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Query Match 78.2%; Score 17.2; DB 4; Length 451;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 CTGCAGCCGCCACCTCTTCTCC 22
Db 301 CAGCAGCCGCCACCATCTTCC 322
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RESULT 11
US-09-614-124B-1647
Sequence 1647, Application US/09614124B
Patent No. 6630574
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fangier, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darriack
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.478C9
CURRENT APPLICATION NUMBER: US/09/614,124B
CURRENT FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 1668
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1647
LENGTH: 451
TYPE: DNA
ORGANISM: Homo sapiens
US-09-614-124B-1647
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Query Match 78.2%; Score 17.2; DB 4; Length 451;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 CTGCAGCCGCCACCTCTTCTCC 22
Db 301 CAGCAGCCGCCACCATCTTCC 322
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RESULT 12
US-09-671-325-1647
Sequence 1647, Application US/09671325
Patent No. 6667154
GENERAL INFORMATION:
APPLICANT: Bangur, Chaitanya S.
```

APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Derrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C12
CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1647.
LENGTH: 451
TYPE: DNA
ORGANISM: Homo sapiens
US-09-671-325-1647

Query Match 78.2%; Score 17.2; DB 4; Length 451;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCAGCCGCCACCTCTTCTCC 22
Db 301 CAGCAGCCGCCACCATCTCC 322

RESULT 13
US-09-658-824-1647
Sequence 1647, Application US/09658824
Patent No. 6746846
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Derrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.478C11
CURRENT APPLICATION NUMBER: US/09/658,824
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 1788
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1647
LENGTH: 451
TYPE: DNA
ORGANISM: Homo sapiens
US-09-658-824-1647

Query Match 78.2%; Score 17.2; DB 4; Length 451;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCAGCCGCCACCTCTTCTCC 22
Db 301 CAGCAGCCGCCACCATCTCC 322

RESULT 14
US-09-621-976-107
Sequence 107, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent .pm
SEQ ID NO 107
LENGTH: 492
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 257..490
NAME/KEY: sig.peptide
LOCATION: 257..325
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 6.6999980926514
OTHER INFORMATION: seq LCPSICMCSVSLA/CV
US-09-621-976-107

Query Match 78.2%; Score 17.2; DB 4; Length 492;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCAGCCGCCACCTCTTCTCC 22
Db 23 CTGCAGCCGCCACCTCTTCTCC 44

RESULT 15
US-09-621-976-1516
Sequence 1516, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent .pm
SEQ ID NO 1516
LENGTH: 543
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 257..505
NAME/KEY: sig.peptide
LOCATION: 257..325
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 6.6999980926514
OTHER INFORMATION: seq LCPSICMCSVSLA/CV
US-09-621-976-1516

Query Match 78.2%; Score 17.2; DB 4; Length 543;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCAGCCGCCACCTCTTCTCC 22
Db 23 CTGCAGCCGCCACCTCTTCTCC 44

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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 13:15:32 ; Search time 155.956 Seconds
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Title: US-10-085-612A-23

Perfect score: 22
Sequence: 1 ctcgagcccccactctctcc 22

Scoring table: IDENTITY NUC
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Maximum Match 100%

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- 11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*
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- 17: /cgn2_6/prodata/1/pubpna/US10F_PUBCOMB.seq:*
- 18: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	1254	17	US-10-085-612-4
2	20.4	92.7	29560	14	US-10-322-281-791
3	18.8	85.5	1188	15	US-10-369-493-31701
4	18.8	85.5	1599	16	US-10-425-114-22378
5	18.8	85.5	2076	18	US-10-739-930-4643
6	18.8	85.5	2149	17	US-10-767-701-9631
7	18.8	85.5	2765	16	US-10-108-260A-2264
8	18.8	85.5	3096	15	US-10-295-027-775
9	18.8	85.5	3096	15	US-10-295-027-792
10	18.8	85.5	3096	15	US-10-295-027-819
11	18.8	85.5	3096	15	US-10-295-027-894
12	18.8	85.5	37252	13	US-10-087-192-1228

C	13	18.8	85.5	235070	13	US-10-087-192-1990	Sequence 1990, Ap
C	14	18.4	83.6	1164	15	US-10-369-493-43210	Sequence 43210, A
C	15	17.8	80.9	201	17	US-10-741-601-1452	Sequence 1452, Ap
C	16	17.8	80.9	201	17	US-10-741-601-1495	Sequence 1495, Ap
C	17	17.8	80.9	258	18	US-10-425-115-83310	Sequence 83310, A
C	18	17.8	80.9	278	9	US-09-923-876-3761	Sequence 3761, Ap
C	19	17.8	80.9	429	9	US-09-923-876-3761	Sequence 3761, Ap
C	20	17.8	80.9	506	17	US-10-767-701-17455	Sequence 2884, Ap
C	21	17.8	80.9	821	17	US-10-437-963-10139	Sequence 17455, A
C	22	17.8	80.9	887	18	US-10-425-115-162309	Sequence 10139, A
C	23	17.8	80.9	1907	16	US-10-425-114-2385	Sequence 162309, A
C	24	17.8	80.9	1960	13	US-10-027-632-53593	Sequence 2385, Ap
C	25	17.8	80.9	1960	15	US-10-027-632-53593	Sequence 53593, A
C	26	17.8	80.9	2041	18	US-10-425-115-174824	Sequence 53593, A
C	27	17.8	80.9	2124	17	US-10-437-963-14264	Sequence 174824, A
C	28	17.8	80.9	3018	13	US-10-027-632-114681	Sequence 14264, A
C	29	17.8	80.9	3018	15	US-10-027-632-114681	Sequence 114681, A
C	30	17.8	80.9	13635	16	US-10-464-368-30	Sequence 114681, A
C	31	17.8	80.9	13635	16	US-10-210-175-13	Sequence 30, Appl
C	32	17.8	80.9	13836	13	US-10-087-192-671	Sequence 671, App
C	33	17.8	80.9	14887	16	US-10-276-774-373	Sequence 671, App
C	34	17.8	80.9	14889	15	US-10-101-510-356	Sequence 373, App
C	35	17.8	80.9	14896	16	US-10-159-563-206	Sequence 356, App
C	36	17.8	80.9	14896	11	US-09-750-972-6	Sequence 206, App
C	37	17.8	80.9	14896	16	US-10-473-974-243	Sequence 6, Appl
C	38	17.8	80.9	14896	18	US-10-052-482-154	Sequence 243, App
C	39	17.8	80.9	32874	16	US-10-087-192-670	Sequence 154, App
C	40	17.8	80.9	104083	13	US-10-087-192-670	Sequence 670, App
C	41	17.4	79.1	201	17	US-10-741-601-1456	Sequence 1456, Ap
C	42	17.4	79.1	201	17	US-10-741-601-1500	Sequence 1500, Ap
C	43	17.4	79.1	201	17	US-10-741-601-10243	Sequence 10243, A
C	44	17.4	79.1	497	17	US-10-767-701-31051	Sequence 31051, A
C	45	17.4	79.1	541	17	US-10-767-701-26731	Sequence 26731, A

ALIGNMENTS

RESULT 1

US-10-085-612-4

Sequence 4, Application US/10085612

Publication No. US20030096251A1

GENERAL INFORMATION:

APPLICANT: Guida, Marco

APPLICANT: Petros, William

APPLICANT: Vredenburg, James

APPLICANT: Colvin, Oliver

APPLICANT: Marks, Jeffrey

TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals

FILE REFERENCE: 4389-5-C1

CURRENT APPLICATION NUMBER: US/10/085,612

CURRENT FILING DATE: 2002-02-26

PRIOR APPLICATION NUMBER: 09/144,367

PRIOR FILING DATE: 1998-08-31

PRIOR APPLICATION NUMBER: 60/271,630

PRIOR FILING DATE: 2001-02-26

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 1254

TYPE: DNA

ORGANISM: Homo sapiens

US-10-085-612-4

Query Match 100.0%; Score 22; DB 14; Length 1254;

Best Local Similarity 100.0%; Pred. No. 9.5;

Matches 22; Conservative 0; Mismatches 0; Gaps 0;

DB 1027 CTCGAGCCCACTCTCTCC 1048

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RESULT 2
US-10-322-281-791
; Sequence 791, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 791
; LENGTH: 29560
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) ... (29560)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-791

Query Match      92.7%; Score 20.4; DB 17; Length 29560;
Best Local Similarity 95.5%; Pred. No. 27;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CTGAGGCCCCACCTCTCTCTCC 22
Db      23106 CAGCAGCCCACTCTCTCTCC 23127

RESULT 3
US-10-369-493-31701/C
; Sequence 31701, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 31701
; LENGTH: 1188
; TYPE: DNA
; ORGANISM: Rhodobacter sphaeroides
US-10-369-493-31701

Query Match      85.5%; Score 18.8; DB 15; Length 1188;
Best Local Similarity 90.9%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGAGGCCCACTCTCTCTCC 22
Db      1056 CTGAGGCCCACTCTCTCTCC 1035

RESULT 4
US-10-425-114-22378
; Sequence 22378, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
```

```
APPLICANT: Zhou, Yihua
APPLICANT: Kovacic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 22378
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3478-020-C3_FLI
US-10-425-114-22378

Query Match      85.5%; Score 18.8; DB 16; Length 1599;
Best Local Similarity 90.9%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGAGGCCCACTCTCTCTCC 22
Db      864 CCGAGCAGCAGCCTCTCTCTCC 885

RESULT 5
US-10-739-930-4643/C
; Sequence 4643, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovacic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 4643
; LENGTH: 2076
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; OTHER INFORMATION: Clone ID: TRIAE-23APR03-CLUSTER29141_1
US-10-739-930-4643

Query Match      85.5%; Score 18.8; DB 18; Length 2076;
Best Local Similarity 90.9%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGAGGCCCACTCTCTCTCC 22
Db      253 CTGAGGCCCACTCTCTCTCC 232

RESULT 6
US-10-767-701-9631
; Sequence 9631, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 9631
; LENGTH: 2149
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TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-26MAY03-CLUS7_1
US-10-767-701-9631

Query Match 85.5%; Score 18.8; DB 17; Length 2149;
Best Local Similarity 90.9%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCACTCTCTTCC 22
DB 1414 CCGCAGCAGCACCTCTCTCC 1435

RESULT 7
US-10-108-260A-2264/c
Sequence 2264, Application US/10108260A
Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2264
LENGTH: 2765
TYPE: DNA
ORGANISM: Homo sapiens
US-10-108-260A-2264

Query Match 85.5%; Score 18.8; DB 16; Length 2765;
Best Local Similarity 90.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCACTCTCTTCC 22
DB 893 CTGCAGCCCACTCTCTTCC 872

RESULT 8
US-10-295-027-775/c
Sequence 775, Application US/10295027
Publication No. US2003023350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevezl, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376

PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 775
LENGTH: 3096
TYPE: DNA
ORGANISM: Homo sapiens
US-10-295-027-775

Query Match 85.5%; Score 18.8; DB 15; Length 3096;
Best Local Similarity 90.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCACTCTCTTCC 22
DB 105 CTGCAGCAGCACCTCTCTCC 84

RESULT 9
US-10-295-027-792/c
Sequence 792, Application US/10295027
Publication No. US2003023350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevezl, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 792
LENGTH: 3096
TYPE: DNA

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; ORGANISM: Homo sapiens
US-10-295-027-792

Query Match      85.5%; Score 18.8; DB 15; Length 3096;
Best Local Similarity 90.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGCAGCCCCACCTCTTCTCC 22
      ||||| ||||| ||||| |||||
Db      105 CTGCAGCAGCACCTCTTCTCC 84

RESULT 10
US-10-295-027-819/c
; Sequence 819, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevez, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT FILING DATE: 2002-11-13
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 819
; LENGTH: 3096
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-819

Query Match      85.5%; Score 18.8; DB 15; Length 3096;
Best Local Similarity 90.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGCAGCCCCACCTCTTCTCC 22
      ||||| ||||| ||||| |||||
Db      105 CTGCAGCAGCACCTCTTCTCC 84

RESULT 11
US-10-295-027-894/c
; Sequence 894, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevez, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT FILING DATE: 2002-11-13
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 894
; LENGTH: 3096
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-894

Query Match      85.5%; Score 18.8; DB 15; Length 3096;
Best Local Similarity 90.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGCAGCCCCACCTCTTCTCC 22
      ||||| ||||| ||||| |||||
Db      105 CTGCAGCAGCACCTCTTCTCC 84

RESULT 12
US-10-087-192-1228/c
; Sequence 1228, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
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SEQ ID NO 1228
LENGTH: 37252
TYPE: DNA
ORGANISM: Homo sapiens
US-10-087-192-1228

Query Match 85.5%; Score 18.8; DB 13; Length 37252;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGAGCCCACTCTCTTCC 22
DB 36114 CTCCTGCCCACTCTCTTCC 36093

RESULT 13
US-10-087-192-1990/C
Sequence 1990, Application US/10087192
Publication No. US2002182586A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 52945200122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1990
LENGTH: 235070
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(235070)
OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1990

Query Match 85.5%; Score 18.8; DB 13; Length 235070;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGAGCCCACTCTCTTCC 22
DB 205859 CTGAGCCCACTCTCTTCC 205838

RESULT 14
US-10-369-493-43210/C
Sequence 43210, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfang
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 43210
LENGTH: 1164
TYPE: DNA

ORGANISM: Myxococcus xanthus
US-10-369-493-43210

Query Match 83.6%; Score 18.4; DB 15; Length 1164;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCAGCCCACTCTCTTCC 22
DB 988 GCAGCCCACTCTCTTCC 969

RESULT 15
US-10-741-601-1452
Sequence 1452, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: CL001500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1452
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-10-741-601-1452

Query Match 80.9%; Score 17.8; DB 17; Length 201;
Best Local Similarity 90.5%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCAGCCCACTCTCTTCC 22
DB 159 TGCAGCCCACTCTCTTCC 179

Search completed: January 26, 2005, 18:15:53
Job time: 157.956 secs

This page Blank (uspto)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 11:30:01 ; Search time 28.7 Seconds
(without alignments)
520.089 Million cell updates/sec

Title: US-10-085-612A-24

Sequence: 1 ctgcagcccgccctctc 21

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCtUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	17.8	84.8	1345	3	US-09-372-339-1	Sequence 1, Appli
2	17.8	84.8	1345	3	US-09-372-339-2	Sequence 2, Appli
3	17.8	84.8	1345	4	US-09-144-367-3	Sequence 3, Appli
4	17.4	82.9	3545	3	US-08-480-474-10	Sequence 10, Appli
5	16.8	80.0	189	4	US-09-270-767-29245	Sequence 29245, A
6	16.8	80.0	743	4	US-09-270-767-13305	Sequence 13305, A
7	16.8	80.0	2464	1	US-07-863-169A-4	Sequence 4, Appli
8	16.8	80.0	2464	2	US-08-429-964-4	Sequence 4, Appli
9	16.8	80.0	2464	3	US-07-935-087-4	Sequence 4, Appli
10	16.8	80.0	2464	5	PCT-US93-08062-4	Sequence 4, Appli
11	16.8	80.0	5574	4	US-09-917-254-40	Sequence 40, Appli
12	16.8	80.0	7453	4	US-09-620-312D-248	Sequence 248, App
13	16.8	80.0	7501	4	US-09-620-312D-249	Sequence 249, App
14	16.8	80.0	7596	4	US-09-023-655-1463	Sequence 1463, Ap
15	16.8	80.0	31571	1	US-08-323-443B-1	Sequence 1, Appli
16	16.8	80.0	53526	3	US-08-658-136-2	Sequence 2, Appli
17	16.8	80.0	53577	3	US-08-658-136-1	Sequence 1, Appli
18	16.4	78.1	677	3	US-08-896-164-42	Sequence 42, Appli
19	16.4	78.1	1347	3	US-08-896-164-84	Sequence 84, Appli
20	16.4	78.1	2297	4	US-09-799-451-689	Sequence 689, App
21	16.4	78.1	2630	3	US-08-669-286-6	Sequence 6, Appli
22	16.4	78.1	2630	3	US-09-469-253-6	Sequence 6, Appli
23	16.4	78.1	2630	3	US-09-642-146-6	Sequence 6, Appli
24	16.4	78.1	8931	3	US-09-051-019-1	Sequence 1, Appli
25	16.2	77.1	59	2	US-08-797-689-26	Sequence 26, Appli
26	16.2	77.1	59	4	US-09-984-186-26	Sequence 26, Appli
27	16.2	77.1	60	2	US-08-797-689-7	Sequence 7, Appli

c	28	16.2	77.1	60	2	US-08-797-689-27	Sequence 27, Appli
c	29	16.2	77.1	60	4	US-09-984-186-7	Sequence 7, Appli
c	30	16.2	77.1	60	4	US-09-984-186-27	Sequence 27, Appli
c	31	16.2	77.1	120	4	US-09-270-767-26922	Sequence 26922, A
c	32	16.2	77.1	288	4	US-08-797-689-9	Sequence 9, Appli
c	33	16.2	77.1	288	4	US-09-984-186-9	Sequence 9, Appli
c	34	16.2	77.1	509	4	US-09-621-976-14709	Sequence 14709, A
c	35	16.2	77.1	557	4	US-10-101-464A-168	Sequence 168, App
c	36	16.2	77.1	628	4	US-09-270-767-11361	Sequence 11361, A
c	37	16.2	77.1	681	3	US-08-347-584A-3	Sequence 3, Appli
c	38	16.2	77.1	681	3	US-08-463-682-18	Sequence 18, Appli
c	39	16.2	77.1	750	2	US-08-797-689-3	Sequence 3, Appli
c	40	16.2	77.1	750	4	US-09-984-186-3	Sequence 3, Appli
c	41	16.2	77.1	837	3	US-09-123-492A-3	Sequence 3, Appli
c	42	16.2	77.1	925	4	US-09-311-021-119	Sequence 119, App
c	43	16.2	77.1	936	4	US-09-416-509C-2	Sequence 2, Appli
c	44	16.2	77.1	960	2	US-07-841-591A-1	Sequence 1, Appli
c	45	16.2	77.1	960	5	PCT-US93-02034-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-372-339-1
; Sequence 1, Application US/09372339
; Patent No. 6174684
; GENERAL INFORMATION:
; APPLICANT: Rebeck, Timothy
; TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
; FILE REFERENCE: PENN-0695
; CURRENT APPLICATION NUMBER: US/09/372,339
; CURRENT FILING DATE: 1999-08-11
; EARLIER APPLICATION NUMBER: 60/096,586
; EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-372-339-1

Query Match 84.8%; Score 17.8; DB 3; Length 1345;
Best Local Similarity 90.5%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCGCCCTCTCTC 21
DB 1050 CTGCAGCCCTCTCTCTCTC 1070

RESULT 2
US-09-372-339-2
; Sequence 2, Application US/09372339
; Patent No. 6174684
; GENERAL INFORMATION:
; APPLICANT: Rebeck, Timothy
; TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
; FILE REFERENCE: PENN-0695
; CURRENT APPLICATION NUMBER: US/09/372,339
; CURRENT FILING DATE: 1999-08-11
; EARLIER APPLICATION NUMBER: 60/096,586
; EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-372-339-2

Query Match 84.8%; Score 17.8; DB 3; Length 1345;
Best Local Similarity 90.5%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCGCCTCTTCTC 21
Db 1050 CTCGAGCCCTGCTCTTCTC 1070

RESULT 3

US-09-144-367-3
; Sequence 3, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0)...(0)
US-09-144-367-3

Query Match 84.8%; Score 17.8; DB 4; Length 1345;
Best Local Similarity 90.5%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCGCCTCTTCTC 21
Db 1050 CTCGAGCCCTGCTCTTCTC 1070

RESULT 4

US-08-480-474-10/c
; Sequence 10, Application US/08480474
; Patent No. 6033865
; GENERAL INFORMATION:
; APPLICANT: Daggett, Lorie P.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lu, Chin-Chun
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA ENCODING
; TITLE OF INVENTION: SAME AND USES THEREFOR
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,474
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie

REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9382B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 3545 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-08-480-474-10

Query Match 82.9%; Score 17.4; DB 3; Length 3545;
Best Local Similarity 94.7%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCAGCCCGCCTCTTCTC 21
Db 500 GCAGCCCGCCTCTTCTC 482

RESULT 5

US-09-270-767-29245/c
; Sequence 29245, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29245
; LENGTH: 189
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-29245

Query Match 80.0%; Score 16.8; DB 4; Length 189;
Best Local Similarity 90.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCGCCTCTTCT 20
Db 176 CTGCAGATCCGCTCTTCT 157

RESULT 6

US-09-270-767-13305/c
; Sequence 13305, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13305
; LENGTH: 743
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13305

Query Match 80.0%; Score 16.8; DB 4; Length 743;
Best Local Similarity 90.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCGCCTCTTCT 20

Db 176 CTGCAGATCCGCGCTCTTCT 157

|||||
RESULT 7
US-07-863-169A-4
; Sequence 4, Application US/07863169A
; Patent No. 5420245
GENERAL INFORMATION:
APPLICANT: Brown, Michael S.
APPLICANT: Goldstein, Joseph L.
APPLICANT: Reiss, Yuval
TITLE OF INVENTION: Retriapeptide-Based Inhibitors of Farnesyl
TITLE OF INVENTION: Transferase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/863,169A
FILING DATE: 03-APR-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/822,011
FILING DATE: 19-JAN-1992
CLASSIFICATION: 530
APPLICATION NUMBER: US 07/937,893
FILING DATE: 18-APR-1991
CLASSIFICATION: 530
APPLICATION NUMBER: US 615,715
FILING DATE: 20-NOV-1990
CLASSIFICATION: 530
APPLICATION NUMBER: US 510,706
FILING DATE: 18-APR-1990
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:297/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2464 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-863-169A-4
Query Match 80.0%; Score 16.8; DB 1; Length 2464;
Best Local Similarity 90.0%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 CTGCAGCCCGCTCTTCT 20
Db 2146 CTGCAGCCCGCTCTTCT 2165
RESULT 8
US-08-429-964-4
; Sequence 4, Application US/08429964
; Patent No. 5962243

GENERAL INFORMATION:
APPLICANT: BROWN, MICHAEL S.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: REISS, YUVAL
APPLICANT: JAMES, GUY L.
TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL
TITLE OF INVENTION: TRANSFERASE INHIBITORS
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,964
FILING DATE: 27-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,625
FILING DATE: 16-FEB-1993
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/822,011
FILING DATE: ABANDONED
CLASSIFICATION: 435
APPLICATION NUMBER: PCT/US/91/02650
FILING DATE: 18-APR-1991
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/615,715
FILING DATE: 20-NOV-1990
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/510,706
FILING DATE: 18-APR-1990 (ABANDONED)
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:432/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2464 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-429-964-4
Query Match 80.0%; Score 16.8; DB 2; Length 2464;
Best Local Similarity 90.0%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 CTGCAGCCCGCTCTTCT 20
Db 2146 CTGCAGCCCGCTCTTCT 2165
RESULT 9
US-07-935-087-4
; Sequence 4, Application US/07935087
; Patent No. 6083917
GENERAL INFORMATION:
APPLICANT: BROWN, MICHAEL S.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: REISS, YUVAL

APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Dunwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 656962e1 Nucleic Acids and
FILE REFERENCE: 784CIP28
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PL_genes Version 1.0
SEQ ID NO 248
LENGTH: 7453
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(4362)
US-09-620-312D-248

Query Match 80.0%; Score 16.8; DB 4; Length 7453;
Best Local Similarity 90.0%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 2;

Oy 1 CTGCAGCCCGCCTCTTCT 20
Db 3279 CTGCAGCTCCTCCTCTTCT 3260

RESULT 13
US-09-620-312D-249/c
Sequence 249, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Dunwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 656962e1 Nucleic Acids and
FILE REFERENCE: 784CIP28
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PL_genes Version 1.0
SEQ ID NO 249
LENGTH: 7501
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(4410)
US-09-620-312D-249

Query Match 80.0%; Score 16.8; DB 4; Length 7501;
Best Local Similarity 90.0%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 2;

Oy 1 CTGCAGCCCGCCTCTTCT 20
Db 3327 CTGCAGCTCCTCCTCTTCT 3308

RESULT 14
US-09-023-655-1463/c
Sequence 1463, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1463:
SEQUENCE CHARACTERISTICS:
LENGTH: 7596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9641957
US-09-023-655-1463

Query Match 80.0%; Score 16.8; DB 4; Length 7596;
Best Local Similarity 90.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGAGCGCCGCTCTTCT 20
|||||
Db 3358 CTGAGCTCTCTCTTCT 3339

RESULT 15

US-08-323-443B-1
; Sequence 1, Application US/08323443B
; Patent No. 5654170
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W.
; APPLICANT: LANDES, GREGORY M.
; APPLICANT: BURR, TIMOTHY C.
; APPLICANT: CONNORS, TIMOTHY D.
; APPLICANT: DACKOWSKI, WILLIAM R.
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,443B
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, S. Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 0372/0A462
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: PKD1 GENOMIC
; US-08-323-443B-1

Query Match 80.0%; Score 16.8; DB 1; Length 31571;
Best Local Similarity 90.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCAGCGCCGCTCTTCTC 21
|||||
Db 22870 TGCAGCTCTCTCTTCTC 22889

Search completed: January 26, 2005, 13:15:26
Job time : 28.825 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: January 26, 2005, 13:15:32 ; Search time 148.867 Seconds
(without alignment)
810.549 Million cell updates/sec

Title: US-10-085-612A-24

Perfect score: 21
Sequence: 1 ctgcagcccccctctctc 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/prodata/1/pubpna/PCr_NEW_PUB.seq:*
- 3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:*
- 5: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
- 6: /cgn2_6/prodata/1/pubpna/PCrUS_PUBCOMB.seq:*
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- 11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	19.4	92.4	1254	14 US-10-085-612-4	Sequence 4, Appl1
2	18.4	87.6	1142	18 US-10-425-115-95740	Sequence 95740, A
3	17.8	84.8	162	16 US-10-260-238-5770	Sequence 5770, Ap
4	17.8	84.8	235	17 US-10-437-963-39436	Sequence 39436, A
5	17.8	84.8	333	17 US-10-437-963-4246	Sequence 4246, Ap
6	17.8	84.8	907	17 US-10-767-701-9673	Sequence 9673, Ap
7	17.8	84.8	1012	9 US-09-957-997-4	Sequence 4, Appl1
8	17.8	84.8	1080	16 US-10-382-122A-14967	Sequence 14967, A
9	17.8	84.8	1115	17 US-10-437-963-4245	Sequence 4245, Ap
10	17.8	84.8	1286	16 US-10-425-114-25053	Sequence 25053, A
11	17.8	84.8	1294	18 US-10-425-115-33839	Sequence 33839, A
12	17.8	84.8	1345	10 US-09-943-115A-1	Sequence 1, Appl1

13	17.8	84.8	1345	14 US-10-146-575-3	Sequence 3, Appl1
14	17.8	84.8	1345	14 US-10-085-612-3	Sequence 3, Appl1
15	17.8	84.8	1471	18 US-10-425-115-20894	Sequence 20894, A
16	17.8	84.8	2374	15 US-10-094-749-173	Sequence 173, App
17	17.8	84.8	11166	9 US-09-957-997-1	Sequence 1, Appl1
18	17.8	84.8	13035	15 US-10-121-960C-14	Sequence 14, Appl
19	17.8	84.8	15185	15 US-10-121-960C-17	Sequence 17, Appl
20	17.8	84.8	29560	17 US-10-322-281-791	Sequence 791, App
21	17.8	84.8	136284	17 US-10-775-169-149	Sequence 149, App
22	17.8	84.8	227246	17 US-10-322-281-314	Sequence 314, App
23	17.4	82.9	502	9 US-09-783-590-5595	Sequence 5595, Ap
24	17.4	82.9	555	17 US-10-437-963-38151	Sequence 38151, A
25	17.4	82.9	685	17 US-10-767-701-27580	Sequence 27580, A
26	17.4	82.9	1212	18 US-10-193-452-18	Sequence 18, Appl
27	17.4	82.9	1902	18 US-10-193-452-16	Sequence 16, Appl
28	17.4	82.9	2376	17 US-10-437-963-53118	Sequence 53118, A
29	17.4	82.9	3687	17 US-10-437-963-94562	Sequence 94562, A
30	17	81.0	21581	15 US-10-017-161-2041	Sequence 2041, Ap
31	17	81.0	21581	15 US-10-292-798-1687	Sequence 1687, Ap
32	17	81.0	53542	9 US-09-801-574-61	Sequence 61, Appl
33	16.8	80.0	201	17 US-10-741-601-1452	Sequence 1452, Ap
34	16.8	80.0	201	17 US-10-741-601-1495	Sequence 1495, Ap
35	16.8	80.0	326	13 US-10-027-632-267839	Sequence 267839, A
36	16.8	80.0	326	15 US-10-027-632-267839	Sequence 267839, A
37	16.8	80.0	330	18 US-10-425-115-27622	Sequence 27622, A
38	16.8	80.0	425	9 US-09-796-692-5944	Sequence 5944, Ap
39	16.8	80.0	425	14 US-10-040-862-5944	Sequence 5944, Ap
40	16.8	80.0	425	16 US-10-057-475B-5944	Sequence 5944, Ap
41	16.8	80.0	425	16 US-10-154-884B-5944	Sequence 5944, Ap
42	16.8	80.0	425	17 US-10-764-324-5944	Sequence 5944, Ap
43	16.8	80.0	477	10 US-09-918-995-12275	Sequence 12275, A
44	16.8	80.0	489	10 US-09-918-995-26537	Sequence 26537, A
45	16.8	80.0	508	15 US-10-029-386-6894	Sequence 6894, Ap

ALIGNMENTS

RESULT 1
US-10-085-612-4
Sequence 4, Application US/10085612
Publication No. US20030096251A1
GENERAL INFORMATION:
APPLICANT: Guida, Marco
APPLICANT: Hall, Jeff
APPLICANT: Petros, William
APPLICANT: Vredenburgh, James
APPLICANT: Colvin, Oliver
APPLICANT: Marks, Jeffrey
TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
TITLE OF INVENTION: Compositions Therefor
FILE REFERENCE: 4389-5-C1
CURRENT APPLICATION NUMBER: US/10/085,612
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/144,367
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/271,630
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 1254
TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-612-4
Query Match 92.4%; Score 19.4; DB 14; Length 1254;
Best Local Similarity 95.2%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Cy 1 CTGCAGCCCGCTCTCTTC 21
Db 1027 CTGCAGCCCGCTCTCTTC 1047

RESULT 2
US-10-425-115-95740
; Sequence 95740, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 95740
; LENGTH: 1142
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_18829C.1
US-10-425-115-95740

Query Match 87.6%; Score 18.4; DB 18; Length 1142;
Best Local Similarity 95.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CTGAGCGCCGCTCTTCT 20
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Db 519 CTGAGCGCCGCTCTTCT 538

RESULT 3
US-10-260-238-5770
; Sequence 5770, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazedbrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 5770
; LENGTH: 162
; TYPE: DNA
; ORGANISM: Zea mays
US-10-260-238-5770

Query Match 84.8%; Score 17.8; DB 16; Length 162;
Best Local Similarity 90.5%; Pred. No. 3.5e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGAGCGCCGCTCTTCT 21
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Db 1 CTGAGCGCCGCTCTTCT 21

Db 48 CTTCAGCCGCTCTTCT 68

RESULT 4
US-10-437-963-39436/C
; Sequence 39436, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 39436
; LENGTH: 235
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_42977C.1
US-10-437-963-39436

Query Match 84.8%; Score 17.8; DB 17; Length 235;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGAGCGCCGCTCTTCT 21
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Db 209 CTGAGCGCCGCTCTTCT 189

RESULT 5
US-10-437-963-4246/C
; Sequence 4246, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 4246
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_11147C.1
US-10-437-963-4246

Query Match 84.8%; Score 17.8; DB 17; Length 333;
Best Local Similarity 90.5%; Pred. No. 3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGAGCGCCGCTCTTCT 21
|||
Db 36 CTGAGCTCGCGCTTCT 16

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RESULT 6
US-10-767-701-9673/c
; Sequence 9673, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 9673
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS29634_1
US-10-767-701-9673

Query Match      84.8%; Score 17.8; DB 17; Length 907;
Best Local Similarity 90.5%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGCAGCCCGCCTCTCTC 21
        |||||
Db      172 CTGCAGCTCCGCGCCTCTC 152

RESULT 7
US-09-957-997-4
; Sequence 4, Application US/09957997
; Patent No. US20020150915A1
; GENERAL INFORMATION:
; APPLICANT: Berkenstam, Anders
; APPLICANT: Bertilsson, Gran
; APPLICANT: Blomquist, Patrik
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-046001
; CURRENT APPLICATION NUMBER: US/09/957,997
; CURRENT FILING DATE: 2001-09-21
; EARLIER APPLICATION NUMBER: SE 0003393-6
; EARLIER FILING DATE: 2000-09-22
; EARLIER APPLICATION NUMBER: 60/238,895
; EARLIER FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1012
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-957-997-4

Query Match      84.8%; Score 17.8; DB 9; Length 1012;
Best Local Similarity 90.5%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGCAGCCCGCCTCTCTC 21
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Db      962 CTCGAGCTCCGCGCCTCTC 982

RESULT 8
US-10-282-122A-14967/c
; Sequence 14967, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
```

```
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITPA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; CURRENT APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14967
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Bordetella pertussis
US-10-282-122A-14967

Query Match      84.8%; Score 17.8; DB 16; Length 1080;
Best Local Similarity 90.5%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGCAGCCCGCCTCTCTC 21
        |||||
Db      291 CTGCAGCGCGCCTCCATCTC 271

RESULT 9
US-10-437-963-4245/c
; Sequence 4245, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 4245
; LENGTH: 1115
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TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_11146C.1
US-10-437-963-4245

Query Match 84.8%; Score 17.8; DB 17; Length 1115;
Best Local Similarity 90.5%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCGCCTCTCTC 21
Db 191 CTGCAGCTCCGCGCCTCTCTC 171

RESULT 10
US-10-425-114-25053/C
Sequence 25053, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 25053
LENGTH: 1286
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3689-241-G6_FLI
US-10-425-114-25053

Query Match 84.8%; Score 17.8; DB 16; Length 1286;
Best Local Similarity 90.5%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCGCCTCTCTC 21
Db 156 CTTCAGCCCGCCTCTCTC 136

RESULT 11
US-10-425-115-33839/C
Sequence 33839, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 33839
LENGTH: 1294
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_130869C.1
US-10-425-115-33839

Query Match 84.8%; Score 17.8; DB 18; Length 1294;

Best Local Similarity 90.5%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCGCCTCTCTC 21
Db 1146 CTGCAGCCCGCCTCTCTC 1126

RESULT 12
US-09-943-115A-1
Sequence 1, Application US/09943115A
Publication No. US20030017469A1
GENERAL INFORMATION:
APPLICANT: SEQUENOM, Inc.
APPLICANT: Risinger, Carl
APPLICANT: Anderson, Maria
APPLICANT: Lewander, Tommy
APPLICANT: Olaisson, Erik
TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9
FILE REFERENCE: 52459-20021.00
CURRENT APPLICATION NUMBER: US/09/943,115A
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: UK 0021286.0
PRIOR FILING DATE: 2000-08-30
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1345
TYPE: DNA
ORGANISM: Homo sapiens
US-09-943-115A-1

Query Match 84.8%; Score 17.8; DB 10; Length 1345;
Best Local Similarity 90.5%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCGCCTCTCTC 21
Db 1050 CTTCAGCCCTGCTCTCTC 1070

RESULT 13
US-10-146-575-3
Sequence 3, Application US/10146575
Publication No. US20030059800A1
GENERAL INFORMATION:
APPLICANT: Lichter, Jay
APPLICANT: Guido, Marco
TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
FILE REFERENCE: SEQ-12P
CURRENT APPLICATION NUMBER: US/10/146,575
CURRENT FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: US/09/144,367
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 1345
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
NAME/KEY: Other
LOCATION: (0)...(0)
US-10-146-575-3

Query Match 84.8%; Score 17.8; DB 14; Length 1345;
Best Local Similarity 90.5%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCGCCTCTCTC 21
Db 1050 CTTCAGCCCTGCTCTCTC 1070

RESULT 14

US-10-085-612-3
; Sequence 3, Application US/10085612
; Publication No. US20030096251A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Vredenburg, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Marks, Jeffrey
; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
; FILE REFERENCE: 4389-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-612-3

Query Match 84.8%; Score 17.8; DB 14; Length 1345;
Best Local Similarity 90.5%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCGCCCTCTTC 21

Db 1050 CTCAGCCCTGCTCTTC 1070

RESULT 15

US-10-425-115-20894/C
; Sequence 20894, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yinhua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 20894
; LENGTH: 1471
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_119054C.1
US-10-425-115-20894

Query Match 84.8%; Score 17.8; DB 18; Length 1471;
Best Local Similarity 90.5%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCGCCCTCTTC 21

Db 285 CTCAGCCCGCCCTCTTC 265

Search completed: January 26, 2005, 18:15:54
Job time : 149.867 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 13:23:32 ; Search time 103.779 Seconds
(without alignments)
8588.699 Million cell updates/sec

Title: SEQ4-1037G
Perfect score: 1254
Sequence: 1 ggcacacaaagagacatgc.....agcctgtgtcctcctcattc 1254

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents NA: *
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	499.2	39.8	1345	US-09-372-339-2	Sequence 2, Appl1
2	498.8	39.8	1345	US-09-144-367-3	Sequence 3, Appl1
3	497.6	39.7	1345	US-09-372-339-1	Sequence 1, Appl1
4	142	11.3	1707	US-09-023-655-1060	Sequence 1060, Ap
5	128.2	10.2	1599	US-09-023-655-1405	Sequence 1405, Ap
6	122.6	9.8	2059	US-09-023-655-1062	Sequence 1062, Ap
7	107.8	8.6	1659	US-09-583-447A-1	Sequence 1, Appl1
8	102.6	8.2	2759	US-09-144-367-1	Sequence 1, Appl1
9	89	7.1	105	US-09-583-447A-41	Sequence 40, Appl
10	78.8	6.3	106	US-09-583-447A-40	Sequence 39, Appl
11	77.2	6.2	106	US-09-583-447A-39	Sequence 14, Appl
12	72.6	5.8	7218	US-08-232-463-14	Sequence 4, Appl1
13	61.4	4.9	1512	US-08-277-031B-4	Sequence 42, Appl
14	61.2	4.9	106	US-09-583-447A-42	Sequence 12, Appl
15	51	4.1	243	US-09-172-108-12	Sequence 10, Appl
16	51	4.1	265	US-09-172-108-10	Sequence 3, Appl1
17	49.2	3.9	36159	US-09-749-588-3	Sequence 3, Appl1
18	49.2	3.9	36159	US-10-115-687-3	Sequence 5, Appl1
19	48.6	3.9	1192	US-09-583-447A-9	Sequence 3, Appl1
20	48.6	3.9	1349	US-09-583-447A-5	Sequence 3, Appl1
21	48.6	3.9	1515	US-09-583-447A-3	Sequence 3, Appl1
22	48.6	3.9	1633	US-09-583-447A-7	Sequence 11, Appl
23	48.6	3.9	1972	US-09-583-447A-11	Sequence 3, Appl1
24	47.8	3.8	64467	US-09-803-671B-3	Sequence 5, Appl1
25	47.4	3.8	57	US-07-640-473-5	Sequence 24, Appl
26	47.4	3.8	57	US-07-908-317-24	Sequence 24, Appl
27	47.4	3.8	57	PCT-US93-06171-24	Sequence 24, Appl

C	28	46.8	3.7	202001	4	US-09-734-674-3	Sequence 3, Appl1
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C	30	45.6	3.6	283	4	US-09-513-999C-30164	Sequence 30164, A
C	31	45.6	3.6	384	4	US-09-513-999C-30900	Sequence 30900, A
C	32	44.6	3.6	116592	4	US-09-818-512-3	Sequence 3, Appl1
C	33	44.2	3.5	57	1	US-07-640-473-13	Sequence 13, Appl
C	34	44	3.5	13158	2	US-08-687-080-105	Sequence 105, App
C	35	42.6	3.4	57	1	US-07-640-473-7	Sequence 7, Appl1
C	36	42.6	3.4	57	1	US-07-640-473-11	Sequence 11, Appl
C	37	42.6	3.4	57	1	US-07-908-317-26	Sequence 26, Appl
C	38	42.6	3.4	57	5	PCT-US93-06171-26	Sequence 26, Appl
C	39	42.2	3.4	551	3	US-08-896-164-38	Sequence 38, Appl
C	40	41	3.3	57	1	US-07-640-473-9	Sequence 9, Appl1
C	41	40.8	3.3	107820	4	US-09-792-616-1	Sequence 1, Appl
C	42	40	3.2	289	3	US-09-007-005-17	Sequence 17, Appl
C	43	40	3.2	289	3	US-09-244-796-17	Sequence 17, Appl
C	44	38.4	3.1	3286	3	US-09-211-417-2	Sequence 2, Appl1
C	45	38	3.0	786431	4	US-09-751-389-3	Sequence 3, Appl1

ALIGNMENTS

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RESULT 1
US-09-372-339-2
; Sequence 2, Application US/09372339
; Patent No. 6174684
; GENERAL INFORMATION:
; APPLICANT: Redbeck, Timothy
; TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
; FILE REFERENCE: PENN-0695
; CURRENT APPLICATION NUMBER: US/09/372,339
; CURRENT FILING DATE: 1999-08-11
; EARLIER APPLICATION NUMBER: 60/096,586
; EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-372-339-2

Query Match      39.8%; Score 499.2; DB 3; Length 1345;
Best Local Similarity 77.9%; Pred. No. 4.4e+158;
Matches 710; Conservative 0; Mismatches 128; Indels 74; Gaps 6;

QY 402 GGATGACACACAGGGGCCAGCAATCTCAACCAAGTCACTCCACCAATTTCTGTCA 461
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DB 382 GGATGACACACAGGGGCCAGCAATCTCAACCAAGTCACTCCACCAAGTCACTG 441
    |||||
QY 462 CCACATGTCATGACGTAACCTCTGTCAGGTCATGATGAAATTAATCAACAC 521
    |||||
DB 442 CCACATGTCATGACGTAACCTCTGTCAGGTCATGATGAAATTAATCAACAC 501
    |||||
QY 522 TGGCCCTTGAAGAACTCACTCTGTCAGGTCATGATGAAATTAATCAACAC 581
    |||||
DB 502 TATGCCCTTGAAGAACTCACTCTGTCAGGTCATGATGAAATTAATCAACAC 559
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QY 582 TAGAGAGAAATAGCAATAGCACTGTGAGAGGAGATAGAGGACCCAGAGAGAA 641
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DB 560 TAAAGAGAAATAGCAATAGCACTGTGAGAGGAGATAGAGGACCCAGAGAGAA 619
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QY 642 ATGTTACATCTGTGTAGAGAGGTTGTAAGAAAGCTTAATAGAGGAGCTGTCTG 701
    |||||
DB 620 ATGTTACATCTGTGTAGAGAGGTTGTAAGAAAGCTTAATAGAGGAGCTGTCTG 678
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QY 702 GCGGGCTTCCAGAGATGTAGAGATCTTACAGGGGCAACAGTCACTCCAGAGAG 761
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DB 679 TCTGGGTTTGAAGAGATGTAGAGATCTTCTAGGGGGCAACAGTCACTCCAGAG 732
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Qy 882 ATGGCTCCACTTCAGTTCTGATTAAGAACTCAGTTCCTGTGACTCCCTGATTAAGCTGA 941
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Qy 942 TTAAGTTGTTTATGATTTCCCATTAAGAACTCAAGAGGTAAAG-CAAGGGGTGT 1000
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Qy 1001 GTGGATTTCTT----- 1011
Db 967 GTGTGATTTCTTGTCCAACTTCCAAAGTGTGAGAAAGCTTTCCAACTGAGGACAGACA 1026
Qy 1012 -----TGTACTGTGCTGAGCTGAGCCCGCTCTTCTTCAGACATTAACAATTT 1063
Db 1027 GTGGCCCTGTACTGTGGCTGAGCTCCAGCCCTGCTCTTCTCTAGCATTAACAATTC 1086
Qy 1064 CAGAGCTTGAACCTAA-GACTGCTGTGAGAGGCGAGGATGCTCCAGGACAGCCCAAC 1122
Db 1087 CAACAGCTCTACTGAATCACTGTGTGAGGCGAGGAAAGCTTCATGCACATACCCAGC 1146
Qy 1123 AAACAAGACACAGCTGAAAGTAAGACTCAGAGGAGACAGTTGAAGAGGCAAGTGGC 1182
Db 1147 AAAGAGACACAGAGCTGAAGAGAGCTCAGAGAGAGATTAAGTAAAGAAATGAT 1206
Qy 1183 GATGACCTCATCCCAATTTGGCGGTGAAACCTGTCTTCTGTGCTGTCAAGCTGTGT 1242
Db 1207 GATGACCTCATCCCAAGCTTGGCCATGAAACCTGTCTTCTGTGCTGTCAAGCTGTGT 1266
Qy 1243 GCTCCTCTATCT 1254
Db 1267 GCTCCTCTATCT 1278

RESULT 2
US-09-144-367-3
; Sequence 3, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; NAME/KEY: Other
; LOCATION: (0)...(0)
; US-09-144-367-3

Query Match 39.8%; Score 498.8; DB 4; Length 1345;
Best Local Similarity 77.7%; Pred. No. 6.2e-158;
Matches 709; Conservative 1; Mismatches 128; Indels 74; Gaps 6;
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Qy 402 GGATGACACACAGGGCCACGAACTCAACCAAGTCACTCCACCAACATTTCTGTCA 461
Db 382 GGATGACACACAGGGCCACGAACTCAACCAAGTCACTCCACCAACATTTCTGTCA 441
Qy 462 CCACCATGTGTACAGTACCTGCTAGGGTCCAGGGTCCATGAAGTAATTAATACAGAC 521
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Db 442 CCCACTGTGTGACAGACCCCTGTAGGGACAGAGCCATGAAGAGGAACTAGAC 501
Qy 522 TGTGCCCTTAGAGAACTCACTGTGCTAAAGGAAACAGGACAGAAACCCACAAGGGTGG 581
Db 502 TAGGCCCTTAGAGAACTCACTGTGCTTAGAGAAACAGGAGTGGAA--CACAATGGTGG 559
Qy 582 TAGAGAGAAATAGACAAATAGACCTGTGTAGAGGGGATAGAGGACCCAGAGAGAGAA 641
Db 560 TAAAGAGAAATAGAGCAATATAGATTCATGAAGGGGATGAAGATGAGCCAGGGGAGAA 619
Qy 642 ATGGTTACATCTGTGTAGAGAGGTGGTGAAGAAACCTTAATTAAGAGGGTCTGTCTG 701
Db 620 ATGGTTACATCTGTGTAGAGAGGTGGTGAAGAAACCTTAAGAGAA-GGCTGTGTCTG 678
Qy 702 GCTGGGCTTCAAGAGATGTGTAGAGAGTCACTAGGGGGCACAAGTCACTCCAGGACAG 761
Db 679 TCTGGGTTTGAAGAGATGTGTAGAGAGTCTTCTAGGGGGCACAAGCACTCCAG----- 732
Qy 762 GGAATTCATGGGTAAAGATCTGCAAGTGTGGCTGTGGGATGATTTCAAGTATTTCTG 821
Db 733 -----GCATAGGTAAGATCTGTAAGGTGTGGCTTGTGGGATGAATTTCAAGTATTTTG 786
Qy 822 GAATGAAGACAGCCATGAGAAACAAGGCAGGTGAGAGATATTTAAAGGCTTCATCCCA 881
Db 787 GAATGAAGACAGCCATGAGAAACAAGGCAGGTGAGAGATATTTAAAGTATTTATGCCA 846
Qy 882 ATGGCTCCACTTCAGTTCTGATTAAGAACTCAGTTCCTGTGACTCCCTGATTAAGCTGA 941
Db 847 ATGGCTCCACTTCAGTTCTGATTAAGAACTCAGTTCCTGTGACTCCCTGATTAAGCTGA 906
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Db 967 GTGTGATTTCTTGTCCAACTTCCAAAGTGTGAGAAAGCTTTCCAACTGAGGACAGACA 1026
Qy 1012 -----TGTACTGTGCTGAGCTGAGCCCGCTCTTCTTCAGACATTAACAATTT 1063
Db 1027 GTGGCCCTGTACTGTGGCTGAGCTCCAGCCCTGCTCTTCTCTAGCATTAACAATTC 1086
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Db 1147 AAAGAGACACAGAGCTGAAGAGAGACTCAGAGGAGAGATTAAGTAAAGAAATGAT 1206
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Db 1207 GATGACCTCATCCCAAGCTTGGCCATGAAACCTGTCTTCTGTGCTGTCAAGCTGTGT 1266
Qy 1243 GCTCCTCTATCT 1254
Db 1267 GCTCCTCTATCT 1278
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RESULT 3
US-09-372-339-1
; Sequence 1, Application US/09372339
; Patent No. 6174684
; GENERAL INFORMATION:
; APPLICANT: Rebbeck, Timothy
; APPLICANT: Felix, Carolyn
; TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
; FILE REFERENCE: PENN-0695
; CURRENT APPLICATION NUMBER: US/09/372,339
; CURRENT FILING DATE: 1999-08-11
; EARLIER APPLICATION NUMBER: 60/096,586
; EARLIER FILING DATE: 1998-08-14
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NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1345
TYPE: DNA
ORGANISM: Homo sapiens
US-09-372-339-1

Query Match 39.7%; Score 497.6; DB 3; Length 1345;
Best Local Similarity 77.7%; Pred. No. 1.6e-157;
Matches 709; Conservative 0; Mismatches 129; Indels 74; Gaps 6;

QY 402 GGATGACACACAGGGGCCAGCAATCCACCAAGTCACTCCACCAATTTCTGTCTCA 461
DB 382 GGATGACATAGACAGGCCCAAGCAATCTCAGCTAAGTCACTCCACCAAGTCTGTCT 441
QY 462 CCCACCATGTGTACAGTACCTCTCTAGGGTCCAGGGTCAATGAAAGTAAATATACAGAC 521
DB 442 CCCACTGTGTACAGACCTCTGTAGGGACACAGAGCATGACAGGGAATTAAGCTAGAC 501
QY 522 TGTGCTTGAAGACCTCACTCTCTCTAAGGAAACAGGACCAAGGAGGAGGAGGAGGAGG 581
DB 502 TATGCCCTTGAAGAGCTCCTCTCTCTCAGGAAACAGGAGGAGGAGGAGGAGGAGGAGG 559
QY 582 TAGAGAGAAATAGACCAATAGACTGTGTAGGGGGATAGAGGACCCAGAGAGAGAA 641
DB 560 TAAAGAGAAAGAGACCAATAGATTCATGAAAGGAGTGAAGAGTCCAGAGGAGAGAA 619
QY 642 ATGGTACATCTGTGTAGAGAGGTTGTGAAGAAAGCTTAAATAGAGGGGTCTGTCTG 701
DB 620 ATGGTACATCTGTGTAGAGAGGTTGTGTAGAGAAAGACTTAAGAGAA-GGCTCTGTCTG 678
QY 702 GCTGGGCTTGAAGAGAGTGTAGAGTCACTAGGGGGCAAGTAACTCCAGGAGAG 761
DB 679 TCTGGGTTTGAAGAGTGTAGAGTCTTCTAGGGGGCAAGGAGCACTCCAG----- 732
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DB 733 -----GCATAGTAAAGATCTGTAGGTGTGCTTGTGTGGATGAATTTCAAGATTTTCTG 786
QY 822 GAATGAAGACAGCCATGAGAAACAGGGCAGGTGAGAGATATTTAAGAGGCTTCATGCCA 881
DB 787 GAATGAGACAGCCATGAGAAACAGGGCAGGCAAGAGGCAATTTAATAGATTTATATCCA 846
QY 882 ATGGCTTCACTTCAATTTCTGATTAAGAACTCAAGTTCCTGTGAGTCTCCTGATTAAGTGA 941
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DB 907 TTAAGTTGTTATGATTCCTCATGAATATGAATCAAGAGAGGATAGTGAAGTGTGTGT 966
QY 1001 GTGCGATTTCTT----- 1011
DB 967 GTGCGATTTCTTGTGCAACTTCAAGGTGAGAGAGCTCTTCAACTGACAGGACAGACACA 1026
QY 1012 -----TCTACTGTGCTGACGTGACGCCGCCCTCTCTTCTTCTCAGACATTAACATTT 1063
DB 1027 GGTGGCCCTGCTACTGTGCTGACGTGACGCCCTCTCTTCTTCTCAGATTAATTAACATC 1086
QY 1064 CAGACAGTTGACCTTAA-GACTGTGTGACAGGAGGAGGAGTCTCAGGACAGACAGCCAGC 1122
DB 1087 CAGACAGCTTCACTGAATCACTGCTGTGACAGGAGGAGGAGGAGTCTCAGATTAACATCAGC 1146
QY 1123 AAAACAAGACACAGCTGAAGTGAAGTCAAGAGAGACAGTTGAAGAGGAGCAAGTGC 1182
DB 1147 AAAGAGCAACACAGAGTGAAGAGTCAAGAGAGAGATTAAGTGAAGAGAGTGT 1206
QY 1183 GATGAGCTCATCCCAATTTTGGCGGTGAGAACTGTGCTTCTCTGCTGTCAAGCTGTGT 1242
DB 1207 GATGAGCTCATCCCAACTTGGCCATGAGAACTGTGCTTCTCTGCTGTCAAGCTGTGT 1266
QY 1243 GCTCCTCTATCT 1254

DB 1267 GCTCCTCTATCT 1278

RESULT 4
US-09-023-655-1060
Sequence 1060, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE.
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-4166
TELEFAX: (650) 855-0555
INFORMATION FOR SEQ ID NO: 1060:
SEQUENCE CHARACTERISTICS:
LENGTH: 1707 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g181345
US-09-023-655-1060
Query Match 11.3%; Score 142; DB 4; Length 1707;
Best Local Similarity 93.7%; Pred. No. 4.2e-37;
Matches 148; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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QY 1157 GGAACAGTTGAAGAGGCAAGTGGGATGGAACCTCATCCCAATTTGGCGGTGAAACC 1216
DB 61 GAACACAGTTGAAGAGGCAAGTGGGATGGAACCTCATCCCAATTTGGCGGTGAAACC 120
QY 1217 TGGCTTCTCTGCTGTCAAGCTGTGTGCTCTCTATCT 1254
DB 121 TGGCTTCTCTGCTGTCAAGCTGTGTGCTCTCTATCT 158
RESULT 5
US-09-023-655-1405
Sequence 1405, Application US/09023655

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; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1405:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1599 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g438625
; US-09-023-655-1405

Query Match          10.2%; Score 128.2; DB 4; Length 1599;
Best Local Similarity 94.3%; Pred. No. 1.9e-32;
Matches 133; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY      1174 GCAAGTGGCGATGAGACTCATCCCAAAATTGGCGGTGAAAACCTGGCTTCTCTGGCTGT 1233
DB      62 GAAAGTGGCGATGAGACTCATCCCAAAATTGGCGGTGAAAACCTGGCTTCTCTGGCTGT 121
QY      1234 CAGCTGTGTCTCTCTATCT 1254
DB      122 CAGCTGTGTCTCTCTATCT 142

RESULT 6
US-09-023-655-1062
; Sequence 1062, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
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; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1062:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2059 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g181373
; US-09-023-655-1062

Query Match          9.8%; Score 122.6; DB 4; Length 2059;
Best Local Similarity 85.1%; Pred. No. 1.8e-30;
Matches 137; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY      1094 GCAGGATGCTCCAGGAGACAGCCCAAGCAACACAGACACAGCTGAAAGTAAGATC 1153
DB      1 GCAGGAAAGCTCCATGACATAGCCCAAGCAACACAGAGCTGAAAGGAAGACTC 60
QY      1154 AGAGGAGACAGTTGAAGAAGGCAAGTGGAGTGCATCCCAATTGGGGGTGAA 1213
DB      61 AGAGGAGAGAGTAAGTAAGAAAGTAGTATGCTCTCATCCAGCTTGSCCATGAA 120
QY      1214 ACCTGGCTTCTCTGCTGTCAAGCTGAGTGTCTCTATCT 1254
DB      121 ACCTGGCTTCTCTGCTGTCAAGCTGAGTGTCTCTATCT 161

RESULT 7
US-09-583-447A-1
; Sequence 1, Application US/09583447A
; Patent No. 6645745
; GENERAL INFORMATION:
; APPLICANT: WOJNOWSKI, Leszek
; APPLICANT: GELINER, Klaus
; APPLICANT: EISELT, Regina
; TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
; FILE REFERENCE: 310115.401
; CURRENT APPLICATION NUMBER: US/09/583,447A
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 1659
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (105) .. (1616)
US-09-583-447A-1
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Query Match	8.6%	Score 107.8;	DB 4;	Length 1659;
Best Local Similarity	76.0%	Pred. No. 1.5e-25;		
Matches 133; Conservative	0;	Mismatches 42;	Indels 0;	Gaps 0;

Qy	1080	GACCTCTGTGCAGGSCAGGSGATGTCACAGSCAGCAGCCAGCAACACAGCAGCAGC	1139
Db	1	GACCTCTGGSCAGAAACAAAGCTCTAATGCAAGCCAGCAAGAGCAGCAGCAGC	60

QY 1140 TGAAGTAGACCTCAGAGAGACAGTTGAGAAAGCCAGTGGCCATGACCTCATCCCA 1199
Db 61 TGAAGAAACTCAGAGACAGAGCTGAAAAAGAAACTGTGTATGGATCTCATTTCCA 120

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Oy      1200  ATTTGGGGGTGAAACCTGGCTTCTCCTGGCTGCAGCCTGGTCTCTCTACT 1254
          |||||
Db      121   ACTTTCATGAAACATGGGTTCTTGTTGCTACAGCCTGGTACTCCTTAAT 175

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RESULT 8
US-09-144-367-1
; Sequence 1, Application US/09144367

Query Match	8.2%	Score 102.6	DB 4	Length 2759
Best Local Similarity	85.7%	Pred. No. 1.3e-23		
Matches 114	Conservative 0	Mismatches 19	Indels 0	Gaps 0

1122 CAAACACGACACAGCTGAAGTAAAGCTCAGAGGAGACATTGAAAGGCAAGTCG 1181
 Oy
 8 CAAAGAGCACACAGAGCTGAAGGAGAGCTCAGAGGAGAGAGATTAAGTAAAGGAAATG 67
 Db

Oy 1182 CGATGACCTCATCCCAATTTGGCGGTGGAACCTGCTTCTCTGCTGTCAAGCTTG 1241
 Db 68 TGAATGGCTTCATCTCCAGACTTGGCCATGGAAACCTGGCTTCTCTGCTGTAGAGCTTG 127

RESULT 9
US-09-583-447A-41
; Sequence 41, Application US/09583447A
; Patent No. 6645745
; GENERAL INFORMATION:
; APPLICANT: WOUNOWSKI, Leszek
; APPLICANT: GELLNER, Klaus

```

1  APPLICANT: EISELT, Regina
2  TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
3  TITLE OF INVENTION: (CYP3A) GENE FAMILY: CYP3AX
4  FILE REFERENCE: 310115.401
5  CURRENT APPLICATION NUMBER: US/09/583,447A
6  CURRENT FILING DATE: 2000-05-30
7  NUMBER OF SEQ ID NOS: 45
8  SOFTWARE: Patentin Ver. 2.1
9  SEQ ID NO 41
10 LENGTH: 105
11 TYPE: DNA
12 ORGANISM: Homo sapiens
13 US-09-583-447A-41

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Query Match	7.1%;	Score 89;	DB 4;	Length 105;
Best Local Similarity	90.5%;	Pred. No. 4.7e-20;		
Matches	95;	Conservative	0;	Mismatches 10;
				Indels

1082 CTGCTGTGCAGGGCAGGGATGCTCCAGGCGACAGCCAGCAACACAGCACACAGCTG 1141
 Oy
 1 CTGCTGTGCAGGGCAGGGAGCTCCAGGCGAACAGCCAGCAACAGCAGCACTCAGCTA 60
 Db

QY 1142 AAAGTAAGACTCAGAGGACAGTTGAGAGGCAAGTGGCATG 1186
 |||||
 Db 61 AAAGTAAGACTCAGAGGACAGTTGAGAGGCAAGTGGCATG 105

RESULT 10
US-09-583-447A-40
; Sequence 40, Application US/09583447A

Query Match	6.3%;	Score 78.8;	DB 4;	Length 106
Best Local Similarity	84.0%;	Pred. No. 1.4e-16;		
Matches	89;	Conservative	0;	Mismatches 17;
				Indels

Oy 1081 ACTGCTGTGCAGGGGACGGAGTGTCTCCAGGCAGACAGCCAGCAAAACAACGACACACAGCT 1140
 Db 1 ACTGCTGTGCAGGGGACGGAGTGTCTCCAGGCAGACAGCCAGCAAAACAACGACACAGCTGCT 60

QY 1141 GAAAGTAACTCAGAGGAGACAGTTGAAGAAGGCAATGGCGATG 1188
 Db 61 GAAAAAAGACTCAGAGGAGAGATTAAGGAAGAAAGTAGTGATG 106

RESULT 11
 US-09-583-447A-39
 Sequence 39, Application US/09583447A
 Patent No. 6645745
 GENERAL INFORMATION:
 APPLICANT: MOJNOWSKI, Leszek
 APPLICANT: GEJLNER, Klaus
 TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
 TITLE OF INVENTION: (CYP3A) GENE FAMILY: CYP3AK
 FILE REFERENCE: 310115.401
 CURRENT APPLICATION NUMBER: US/09/583,447A

CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 39
LENGTH: 106
TYPE: DNA
ORGANISM: Homo sapiens
US-09-583-447A-39

Query Match 6.2%; Score 77.2; DB 4; Length 106;
Best Local Similarity 83.0%; Pred. No. 4.7e-16;
Matches 88; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Db 1081 ACTGCTGTGCGAGGCGAGGATGCTCCAGGCGACAGCCCGCAACACAGACACAGCT 1140
1 ACTGCTGTGCGAGGCGAGGATGCTCCAGGCGACAGCCCGCAACACAGACACAGCT 60
Qy 1141 GAAGTAGACTCAGAGGACAGTGTGAAGAGCAATGGCGATG 1186
Db 61 GAAGGAGACTCAGAGGAGAGATAGTAAAGAAAGTAGTATG 106

RESULT 12

US-08-232-463-14/C
Sequence 14, Application US/08232463
Patent No. 5670367

GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 INMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ5pT-Fls
US-08-232-463-14

Query Match 5.8%; Score 72.6; DB 1; Length 7218;
Best Local Similarity 1.6%; Pred. No. 3.7e-13;

Matches 6; Conservative 240; Mismatches 129; Indels 0; Gaps 0;
Qy 489 GTCGAGGTCATGAAGTAATAATACAGACTGTGCTTGAGGAATCACTGTGCT 548
1439 GTACACRR 1380
Qy 549 AAGGAAACAGACAGAAACCCACAGAGTGTAGAGAGAAATAGACAATAGAGATG 608
1379 RRR 1320
Qy 609 TGTGAGGGGATAGAGGACACCCAGAGGAAATGTTATCTGTGTGAGAGTGTG 668
1319 RRR 1260
Qy 669 TAAGAAAGACTTAATGAAGGGCTGTGCTGCTGCTGCAAGATGTAGAGAT 728
1259 RRR 1200
Qy 729 CATCTAGGGGACACAGTACCTCCAGGACAGGGAATGTGATGTTAAATCTGCAGT 788
1199 RRR 1140
Qy 789 TGTGCTGTGAGGATGATTTCAAGTATCTGGAATGAGACAGCCATGAAACAAGG 848
1139 RRR 1080
Qy 849 CAGGTAGAGATAT 863
Db 1079 RRRRRRRRRRRRRAT 1065

RESULT 13

US-08-277-031B-4
Sequence 4, Application US/08277031B
Patent No. 6620593

GENERAL INFORMATION:
APPLICANT: Hayashi, Koji
APPLICANT: Sakaki, Toshiyuki
APPLICANT: Yabuseki, Yoshiyaeu
APPLICANT: Komai, Koichiro
APPLICANT: Kaneko, Hideo
APPLICANT: Nakatsuka, Iwao
TITLE OF INVENTION: METHOD FOR SAFETY EVALUATION OF
TITLE OF INVENTION: CHEMICAL COMPOUND USING RECOMBINANT YEAST EXPRESSING
NUMBER OF SEQUENCES: 42
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5inch, 1.44MB
COMPUTER: IBM PC
OPERATING SYSTEM: Dos 5.0
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/277,031B
FILING DATE: 19-JULY-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP-201120/1993
APPLICATION NUMBER: JP-180246/1993
APPLICATION NUMBER: JP-208279/1993
FILING DATE: 20-07-1993
FILING DATE: 21-07-1993
FILING DATE: 30-07-1993
ATTORNEY/AGENT INFORMATION:
NAME: Raymond C. Stewart
REGISTRATION NUMBER: 21,066
REFERENCE/DOCKET NUMBER: 20-3530P

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/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 703-205-8000
/ TELEFAX: 703-205-8050
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1512
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ US-08-277-031B-4

Query Match
Best Local Similarity 91.5%; Score 61.4; DB 4; Length 1512;
Matches 65; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1184 ATGACCTCATCCCAATTGGCGGTGAAACCTGCTTCTCTGCTGTCAAGCTGTG 1243
DB 1 ATGGCTCTCATCCAGACTTGGCCATGTGAACCTGCTTCTCTGCTGTCAAGCTGTG 60
QY 1244 CTCCTCTATCT 1254
DB 61 CTCCTCTATCT 71

RESULT 14
US-09-583-447A-42
/ Sequence 42, Application US/09583447A
/ Patent No. 6645745
/ GENERAL INFORMATION:
/ APPLICANT: WOJNOMSKI, Leszek
/ APPLICANT: GELNER, Klaus
/ APPLICANT: BISSET, Regina
/ TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
/ FILE REFERENCE: 310115.401
/ CURRENT APPLICATION NUMBER: US/09/583,447A
/ NUMBER OF SEQ ID NOS: 45
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 42
/ LENGTH: 106
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-583-447A-42

Query Match
Best Local Similarity 73.6%; Score 61.2; DB 4; Length 106;
Matches 78; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1081 ACTGCTGCGAGGCGAGGATGCTCCAGCAGACAGCCGCAAGCAACAGACACAGCT 1140
DB 1 ACCTCTGGGCGAGAAACAAAGCTCTATATGCAAGCCGCAAGAGCAGACACAGCT 60
QY 1141 GAAAGTAAGACTCAGAGAGACAGTGAAGAGCAAGTGGCGATG 1186
DB 61 GAAAGTAAGACTCAGAGAGACAGTGAAGAGCAAGTGGCGATG 106

RESULT 15
US-09-172-108-12
/ Sequence 12, Application US/09172108
/ Patent No. 6160104
/ GENERAL INFORMATION:
/ APPLICANT: Cunningham, Mary Jane
/ APPLICANT: Zweigler, Gary B.
/ APPLICANT: Panzer, Scott R.
/ APPLICANT: Selhammer, Jeffrey J.
/ TITLE OF INVENTION: MARKERS FOR PEROXISOMAL PROLIFERATORS
/ FILE REFERENCE: PA-0012 US
/ CURRENT APPLICATION NUMBER: US/09/172,108
/ CURRENT FILING DATE: 1998-10-13
/ NUMBER OF SEQ ID NOS: 56
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/ SOFTWARE: PERL Program
/ SEQ ID NO 12
/ LENGTH: 243
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: 33
/ OTHER INFORMATION: a or g or c or t, unknown, or other
/ OTHER INFORMATION: 700141708H1
/ US-09-172-108-12
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Query Match
Best Local Similarity 69.7%; Score 51; DB 3; Length 243;
Matches 83; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

QY 1134 CACAGCTGAAAGTAAGACTCAGAGAGACAGTGAAGA-AGGCAAGTGGCGATGACCTC 1192
DB 35 CCCAGCTAGAGGAGACACACAGAGAGTAATTGCTGACAGACCTGCAAGGAGTGAAGCTG 94
QY 1193 ATCCCAATTGGCGGTGAAACCTGCTTCTCTGCTGTGACCTGTGCTCTCTCTA 1251
DB 95 CTTGAGCTCTCAGACTGGAACCTGGGTCTCTCTGAGTGTCTGTGCTCTCTA 153
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
11465.419 Million cell updates/sec

Title: SEQ4-1037G

Perfect score: 1254
Sequence: 1 GGCACACAAGAGACATGTC.....AGCCGTGTCCTCATCT 1254

Scoring table:
Gapop 10.0, Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications NA:*

- 1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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- 11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/1/pubpna/US09D_PUBCOMB.seq:*
- 13: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/prodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/prodata/1/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/prodata/1/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/prodata/1/pubpna/US10I_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1252.4	99.9	1254	14	Sequence 4, Appl
2	664	53.0	8776	16	Sequence 149, App
3	567.4	45.2	8776	16	Sequence 150, App
4	498.8	39.8	1345	14	Sequence 3, Appl
5	498.8	39.8	1345	14	Sequence 3, Appl
6	498.4	39.7	1345	14	Sequence 1, Appl
7	457.2	36.5	13035	15	Sequence 14, Appl
8	434.6	34.7	15185	15	Sequence 17, Appl
9	396.4	31.6	11186	9	Sequence 1, Appl
10	387.2	30.9	1012	9	Sequence 47, Appl
11	253.4	20.2	8943	16	Sequence 48, Appl
12	222.8	17.8	8943	16	Sequence 48, Appl

13	142	11.3	1707	9	US-09-880-107-2114	Sequence 2114, Ap
14	142	11.3	1707	16	US-10-641-643-1060	Sequence 1060, Ap
15	141	11.2	384	9	US-09-925-297-24	Sequence 24, Appl
16	135.6	10.8	2768	15	US-10-268-827-14	Sequence 14, Appl
17	135.6	10.8	2768	15	US-10-388-360-297	Sequence 297, App
18	135.6	10.8	2768	15	US-10-388-360-353	Sequence 363, App
19	128.2	10.2	1599	16	US-10-641-643-1405	Sequence 1405, Ap
20	126.6	10.1	1525	9	US-09-880-107-3816	Sequence 3816, Ap
21	123.8	9.9	2059	15	US-10-641-643-1724	Sequence 1724, Ap
22	122.6	9.8	2059	16	US-10-641-643-1062	Sequence 1062, Ap
23	107.8	8.6	1659	13	US-10-007-814-1	Sequence 1, Appl
24	107.6	8.6	1915	16	US-10-112-944-188	Sequence 188, App
25	103.8	8.3	2849	9	US-09-880-107-2110	Sequence 2110, Ap
26	102.6	8.2	2759	13	US-10-146-575-1	Sequence 1, Appl
27	96.4	7.7	489	14	US-10-027-632-277590	Sequence 277590,
28	96.4	7.7	489	15	US-10-027-632-277590	Sequence 277590,
29	94.8	7.6	2011	15	US-09-880-107-1586	Sequence 1586, Ap
30	89	7.1	105	13	US-10-007-814-41	Sequence 41, Appl
31	78.8	6.3	106	13	US-10-007-814-40	Sequence 40, Appl
32	77.2	6.2	106	13	US-10-007-814-39	Sequence 39, Appl
33	72.8	5.8	240	9	US-09-960-352-15077	Sequence 15077, A
34	72.8	5.8	380	9	US-09-960-352-15107	Sequence 15107, A
35	72.8	5.8	411	9	US-09-960-352-4176	Sequence 4176, Ap
36	72.8	5.8	418	9	US-09-960-352-4657	Sequence 4657, Ap
37	72.8	5.8	422	9	US-09-960-352-6070	Sequence 6070, Ap
38	72.8	5.8	430	9	US-09-960-352-8232	Sequence 8232, Ap
39	71.4	5.7	347	9	US-09-960-352-3467	Sequence 3467, Ap
40	71.4	5.7	442	9	US-09-960-352-1762	Sequence 1762, Ap
41	71.2	5.6	339	9	US-09-960-352-8257	Sequence 8257, Ap
42	70.2	5.6	207	9	US-09-960-352-9871	Sequence 9871, Ap
43	70.2	5.6	404	9	US-09-960-352-7510	Sequence 7510, Ap
44	69.6	5.6	209	9	US-09-960-352-9181	Sequence 9181, Ap
45	66.4	5.3	322	9	US-09-960-352-6312	Sequence 6312, Ap

ALIGNMENTS

RESULT 1
US-10-085-612-4
: Sequence 4, Application US/10085612
: Publication No. US2003096251A1
: GENERAL INFORMATION:
: APPLICANT: Guida, Marco
: APPLICANT: Hall, Jeff
: APPLICANT: Petros, William
: APPLICANT: Vredenburg, James
: APPLICANT: Colvin, Oliver
: APPLICANT: Marks, Jeffrey
: TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
: FILE REFERENCE: 4389-5-C1
: CURRENT APPLICATION NUMBER: US/10/085,612
: CURRENT FILING DATE: 2002-02-26
: PRIOR APPLICATION NUMBER: 09/144,367
: PRIOR FILING DATE: 1998-08-31
: PRIOR APPLICATION NUMBER: 60/271,630
: PRIOR FILING DATE: 2001-02-26
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 4
: LENGTH: 1254
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-085-612-4

Query Match 99.9%; Score 1252.4; DB 14; Length 1254;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1253; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCACACAAGAGACATGTCATGTTCTACTTATTTGGATCTACAAATCAAAACAT 60
DB 1 GGCACACAAGAGACATGTCATGTTCTACTTATTTGGATCTACAAATCAAAACAT 60

QY 61 TGAGCTAATGTCGGGCTTAACTATTTTGTACCCCTAAGTACAGGAGCAGCCATTA 120
DB 61 TGAGCTAATGTCGGGCTTAACTATTTTGTACCCCTAAGTACAGGAGCAGCCATTA 120
QY 121 GAATACATGATGTAATGCTTTAATACAGGAATGAATAGTGAAGGACAGGGTGTGGG 180
DB 121 GAATACATGATGTAATGCTTTAATACAGGAATGAATAGTGAAGGACAGGGTGTGGG 180
QY 181 TGTCTCTGATACATAGTATCTTCTTGACACATTCAGTACAACTCTCAACAGTAAAT 240
DB 181 TGTCTCTGATACATAGTATCTTCTTGACACATTCAGTACAACTCTCAACAGTAAAT 240
QY 241 CTCTTCATGATGTAATGCTTTCTGAGAAATTAAGTGGAGAAACATGCTTCTTATTTTC 300
DB 241 CTCTTCATGATGTAATGCTTTCTGAGAAATTAAGTGGAGAAACATGCTTCTTATTTTC 300
QY 301 CTCTTCAGAAACAAGCAATTCATGATGTTGGGAAACAGTGTGGCTGCATTCAGGCC 360
DB 301 CTCTTCAGAAACAAGCAATTCATGATGTTGGGAAACAGTGTGGCTGCATTCAGGCC 360
QY 361 AAGCAACATTAATGCTATTCATCAACAGACTCAGAGGGATGACACAGGGGCC 420
DB 361 AAGCAACATTAATGCTATTCATCAACAGACTCAGAGGGATGACACAGGGGCC 420
QY 421 AGCAATCTCAACCAAGTCACTCCACCAACATTTCTGTCACCCCATGTGTACATAC 480
DB 421 AGCAATCTCAACCAAGTCACTCCACCAACATTTCTGTCACCCCATGTGTACATAC 480
QY 481 CTTGCTAAGGTCACAGGTCATGAAGTAATTAATACAGACTGTCCTTGAAGAACTCA 540
DB 481 CTTGCTAAGGTCACAGGTCATGAAGTAATTAATACAGACTGTCCTTGAAGAACTCA 540
QY 541 CCTCTGCTAAGGAAACAGGACACAGAAACCAAGGGGTGTAGAGAGAAATAGACAA 600
DB 541 CCTCTGCTAAGGAAACAGGACACAGAAACCAAGGGGTGTAGAGAGAAATAGACAA 600
QY 601 TAGGACTGTGTAGAGGGGATAGAGAGCACCAGAGAGAAATGTTACATCTGTGTAG 660
DB 601 TAGGACTGTGTAGAGGGGATAGAGAGCACCAGAGAGAAATGTTACATCTGTGTAG 660
QY 661 GAGGTTGTGAAGAAACCTTAAATGAAGGGGTCTGTGCTGGGCTTGCAAGATGT 720
DB 661 GAGGTTGTGAAGAAACCTTAAATGAAGGGGTCTGTGCTGGGCTTGCAAGATGT 720
QY 721 GTAGAGTCAATCAGGGGACCAAGTACACTCCAGGACAGGGAATGCAATGGTAAAG 780
DB 721 GTAGAGTCAATCAGGGGACCAAGTACACTCCAGGACAGGGAATGCAATGGTAAAG 780
QY 781 TCTGCAATGTGTGCTGTGGGGATGATTTCAAGTATTTGGAATGAAGACAGCATGA 840
DB 781 TCTGCAATGTGTGCTGTGGGGATGATTTCAAGTATTTGGAATGAAGACAGCATGA 840
QY 841 AAGAAGGGGAGTGAAGAGATTTTAAAGAGCTTCAGTCCAGCTTCAAGTTTC 900
DB 841 AAGAAGGGGAGTGAAGAGATTTTAAAGAGCTTCAGTCCAGCTTCAAGTTTC 900
QY 901 TGATTAAGAACTCAGGTTCCGTGACCTCCATTAATTAAGTGTGTTATGATTC 960
DB 901 TGATTAAGAACTCAGGTTCCGTGACCTCCATTAATTAAGTGTGTTATGATTC 960
QY 961 CCATAGAAATGAATCAAGAGGTGAAGCAAGGGGTGTGCGATTTCTTGTACTGG 1020
DB 961 CCATAGAAATGAATCAAGAGGTGAAGCAAGGGGTGTGCGATTTCTTGTACTGG 1020
QY 1021 CTGCAAGTGAAGCCCGCTCTCTCTCCAGACATTAACATTTCAAGAGCTTGAAG 1080
DB 1021 CTGCAAGTGAAGCCCGCTCTCTCTCCAGACATTAACATTTCAAGAGCTTGAAG 1080
QY 1081 ACTGCTGTGAGAGGACAGGATGCTCCAGGACAGAGCCAGCAACAGACAGACT 1140
DB 1081 ACTGCTGTGAGAGGACAGGATGCTCCAGGACAGAGCCAGCAACAGACAGACT 1140

QY 1141 GAAAGTAAAGCTAGAGGAGACAGTTGAAGAGGCAAGTGGCATGAGCTCATCCCAA 1200
DB 1141 GAAAGTAAAGCTAGAGGAGACAGTTGAAGAGGCAAGTGGCATGAGCTCATCCCAA 1200
QY 1201 TTTGGGGGTGAAGACCGGCTTCTCCTGGCTGACAGCTGTGTCCTCATCT 1254
DB 1201 TTTGGGGGTGAAGACCGGCTTCTCCTGGCTGACAGCTGTGTCCTCATCT 1254

RESULT 2
US-10-257-166-149
; Sequence 149, Application US/10257166
; Publication No. US2004002320A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Method and Nucleic Acid for Analysing the Methylation of
; FILE REFERENCE: 5013.1011
; CURRENT APPLICATION NUMBER: US/10/257,166
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: PCT/EP01/07470
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-06-29
; 2000-06-30
; 2000-09-01
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 149
; LENGTH: 8776
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-257-166-149

Query Match 53.0%; Score 664; DB 16; Length 8776;
Best Local Similarity 73.4%; Pred. No. 9e-207;
Matches 919; Conservative 0; Mismatches 320; Indels 13; Gaps 5;

QY 4 ACAAGAGGACATTCATGCTCTCTCACTTATTTGGGGATCTCAATCAATCAATCAATG 63
DB 3919 AGAAATATGATG 3978
QY 64 GCTAATGCTGGGCTTAACTATTTGTAACCTTAAGTACAGGAGACAGCCATTAGA 123
DB 3979 GTTAATGCTGGGCTTAACTATTTGTAACCTTAAGTACAGGAGACAGCCATTAGA 4037
QY 124 TACATGATGATGCTTTAATACAGGAATGAATGATGATGATGATGATGATGATG 183
DB 4038 TATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4097
QY 184 TCTTCGATACATAGATGATGATGATGATGATGATGATGATGATGATGATGATG 243
DB 4098 TTTTGTGATG 4157
QY 244 TTGATG-TANGTAACTTCTGAGGAATTAAGTGGCAAGCATGCTTCTTATTTTCT 302
DB 4158 TTTATGTTATGTTATTTTATGAGGAATTAAGTGGCAAGCATGCTTCTTATTTTCT 4217
QY 303 TTGCAAGACAGCAATTCATGATGATGATGATGATGATGATGATGATGATGATG 362
DB 4218 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4276
QY 363 GCAACATTAATGCTATATGCTATCAACAGACTCAGAGGGAGAGACACAGGGGCCAG 482
DB 4277 GTTAATTAATGATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 4330
QY 423 CAATCTCACCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 482
DB 4331 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4390

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Qy 483 TGCTAGGTCGACGGTCATGAAATATAATATACAGACTGCTCCCTGAGGAATCACC 542
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4391 TGTTAGGAATTTAGGTTATGAAATATATATATATATATATATATATATATATAT 4450
Qy 543 TCTGCTAAGGAAACAGGCAACAAACCCACAGGCTGTGTAGAGAAATAGACAATA 602
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4451 TTTGTTAAGGAAATAGATATAGAAATTTAAATGCTGTGTAGAGAAATAGACAATA 4510
Qy 603 GGCATGCTGAGGGGATAGAGGACCCAGAGGAAATGTATACATGTGTGAGGA 662
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4511 GGAATGTGTAGGGGATAGAGGATATTTAGAGGAAATGTTATATTTGTGTAGGA 4570
Qy 663 GGTGTGTAAGAAAGACTTTAATAGAAAGGCTGTGTGCTGCTGCTGCAAGATGTGT 722
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4571 GGTGTGTAAGAAATTTAATAGTAAGGCTTTGTTGTGTGCTTTGGAAGATACGT 4630
Qy 723 AGGATCATCTAGGGGCAACATCACTCCAGGCAAGGAAATTCATGGGTAAAGATC 782
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4631 AGGATTAATTTAGAGGCTATAGGTATTTTATAGGTAGAGGAAATTCGTGGTAAAGATG 4690
Qy 783 TGCACTGTGCTGTGAGGATAGATTTCAAGTATTCGAAATGAAGACAGCCATGAGAA 842
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4691 TGATGCTGTGTGTGTAGAGATGATTTTATATTTTATAGATGAAGGTATAGT-- 4747
Qy 843 CAAGGCAAGGTGAGAGGATATTTAAGAGGCTTCATGCCAATGCTCCACTTCAGTTCTG 902
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4748 -AGGGGATGAGTGAAGAGGCTTAATAGATTTTATATGTTAATGTTTATGAGTTTGG 4806
Qy 903 ATAGAATCTAGGTTCCGTGACTCCCTGATAAATCTGATTAAGTTGTTATGATCCCC 962
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4807 ATAGAATTTAGAAATTTTGTGATTTTCGATTAATATGATTAAGTTTATGATTTTTC 4866
Qy 963 ATGAATATTAATCTCAAGAGGTAAGCAAGGCTGTGTGCTGCTGCTGCTGCTGCTGCT 1022
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4867 ATGAATATTAATTTAAAGAGGTATGATTAAGGCTGTGTGCTGCTGCTGCTGCTGCTG 4926
Qy 1023 GCAGCTGCAACCCGCTCTCTCCAGCACATTAACATTTTACAGCAGCTTGAACCTAAGAC 1082
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4927 GTAGTTATATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 4986
Qy 1083 TGCTGTGCAAGGCAAGGATCTCCAGGCAAGCAGCCAGCAACAGACACACAGCTGA 1142
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4987 TGTTGTGTAGGTAAGGAGATTTTATAGTTAATAGTTAATAGTTAATAGTTAATAGTTA 5046
Qy 1143 AAGTAAGCTCAAGAGGACAGTTGAAGAGGCAAGTGTGCAATGCACTCATCCCAATT 1202
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5047 AAGGAATTTAATAGAAATATAGTTGAAGAGGAAAGTGGCGATGATTTTATTTTAAATT 5106
Qy 1203 TGCGGCTGAAACCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1254
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5107 TGCGGCTGAAATTTGCTTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 5158

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; SEQ ID NO 150
; LENGTH: 8776
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: chemically created genomic DNA (Homo sapiens)
US-10-257-166-150

Query Match      45.2%; Score 567.4; DB 16; Length 8776;
Best Local Similarity 68.6%; Pred. No. 6.2e-175;
Matches 859; Conservative 0; Mismatches 381; Indels 13; Gaps 5;

Qy 3 CACACAAAGAGACATTCAGATGTTCTCATCTATTTGTGGATCTCAAAATCAAAATTC 62
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4859 CAAACAAACAAATATTAACAAATTCACATCTTATTAATCTTCAAAATCAAAATTC 4800
Qy 63 AGCTAATGCTGGCTCTTACTCAATTTGTACCTTAAGTACAGGAGCACAGCATTTAGA 122
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4799 AACTAATATCTAAACCTTAATCAATATTAATACCC-AAATCTAATAACACACACTTTTAA 4741
Qy 123 ATACATGATGATGCTTTAATACAGAAATAGTAGAGGACAGGGGTGGTG 182
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4740 ATACATCATTAATCTTTAATACAAATATTAATTAATTAATTAATTAATTAATTA 4681
Qy 183 TTCTTCTGATATACATAGTATCTCTTGAACATTCAGTACATCTTCACAGGTAAGTCT 242
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4680 TTCTTCTAATACATATCTTCTTACCAATTCATTAACATCTTCACAAATTAATCT 4621
Qy 243 CTTCAT- GATGTTACCTCTGAGAAATTAAGTGGCAACATGCTCTTATTTTCC 301
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4620 CTTCATTTATTTATCTTACTTTAATAAATTAATTAACAAACATTAATTTCTATTTTCC 4561
Qy 302 TTTCGAGAAACAAACCAATTCGATTAGTGGGAAACAGTCTGCTGCTGCTGCTGCTGCTG 361
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4560 TTTCGAGAAACAAACCAATTTATTAATTAACAAAT-ATAATCAATTTAATTTCCA 4502
Qy 362 AGCAACCATTAATGCTATGCTATCACACAGCTCAGAGGGATGACACAGGGGCCA 421
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4501 AACACATTAATCTATTTACTATCACACAAATTAATTAATTAATTAATTAATTAATTA 4448
Qy 422 GCAATCTACCCAGTCACTCCACCAATTTCTGTGTCACCCAGTGTACAGTACC 481
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4447 ACAATCTACCCCAAAACCAATCTCAACCAATTTCTAATTTACCAACATTAATTAATTA 4388
Qy 482 CTGCTAGGCTCAGGCTCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 541
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4387 CTACTAATAAACAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4328
Qy 542 CTCTGCTAAGGAAACAGGACAGAAACCCACAAAGGTGTAGAGAGAAATAGACAAAT 601
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4327 CTCTACTAATAAACAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4268
Qy 602 AGGACTGTGTGAGGGGATAGAGGACCCAGAGAGAGAAATGTTATCATCTGTGAGG 661
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4267 AAAACATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4208
Qy 662 AGGTGTGTAAGAAAGACTTATTAAGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 721
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4207 AAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4148
Qy 722 TAGAGTCACTAGGGGCAACAGTACCTCCAGGCAAGGAAATTCATGGGTAAAGAT 781
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4147 TAAATATCATCTAATAAACAATAATCACTCCAAACAAATAAATTCGTAAATTAATTA 4088
Qy 782 CTGCACTGTGCTGTGAGGATGATTTCAAGTATTCGAAATGAAGACAGCCATGAGAA 841
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4087 ATATAATATTAATCTTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4028
Qy 842 ACAAGGCAAGTGAAGGATTTAAGAGCTTCATGCGAAATGCTCACTTCAGTTCT 901
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4027 AAA-----CAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATTC 3972
Qy 902 GATTAAGAACTCAGGTTCCGTGACTCCCTGATTAATTAATTAATTAATTAATTAATTC 961

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Db 3971 AATTAACCAACCAACCTTAACCTCCCGATTAACCTTAATTAACCTTTTCAATAATTCCT 3912
Qy 962 CATAGATATGAACTCAAGAGGTAAAGCAAAAGGGGTGTGCGATTCTTTGCTACTGGC 1021
Db 3911 CATTAACATTAACCTCAAAAAAATCAACAAAAAATATAGATTCTTTACTATTAAC 3852
Qy 1022 TCGAGCTGACGCCCGCTCTCTCTCAAGCATTAACATTTGACGACTTGACCTTAAGA 1081
Db 3851 TACAACATTAATACCTTACTCTCTCTCAAGCATTAATCTTTCAACAACTTAATAAAA 3792
Qy 1082 CTGCTGTCAGGGAGGAGTCTCCAGGACAGCCCGAACAACAGACACACACTG 1141
Db 3791 CTACTATTAACAAACAAAAAACTCAACAAACCAACCAACCAACCAACACTCACTA 3732
Qy 1142 AAGTAAGCTCAGAGAGACAGTGAAGAAAGCAAGTGGGAGTGAAGCTTCACTCCAAT 1201
Db 3731 AAAAAAACTCAACAAACCAATTAATAAAAAAATTAACGATTAACCTTCACTCCAAT 3672
Qy 1202 TTGGCGGTGAAACCTGCTTCTCTGCTGTCAGCCTGCTCTCTATCT 1254
Db 3671 TTAACGATTAACAACTTACTCTCTCACTATCACTAATTAATCTCTATCT 3619
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RESULT 4
US-10-146-575-3
; Sequence 3, Application US/10146575
; Publication No. US20030059800A1
; GENERAL INFORMATION:
; APPLICANT: Lichner, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/10/146,575
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US/09/144,367
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0)...(0)
; US-10-146-575-3
```

```
Query Match 39.8%; Score 498.8; DB 14; Length 1345;
Best Local Similarity 77.7%; Pred. No. 8.4e-153;
Matches 709; Conservative 1; Mismatches 128; Indels 74; Gaps 6;
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Qy 402 GGATGACACAGAGGGCCGCAATCTCACCCAAAGTCACTCCACCAATTTCTGTGCA 461
Db 382 GGATGACATAGACAGGCCCGCAATCTCAAGTAACTCCACGCTTTTAAGTTG 441
Qy 462 CCCACATGTGTACAGTACCTCTGTAGAGTTCAGAGGTCAAGAAAGTAAATATATACAGAC 521
Db 442 CCCACTGTGTACAGACCTCTGTAGAGACAGAGCATGACAGGAAATAGACTAGAC 501
Qy 522 TGTGCTTGTAGAACTCACTCTGTCTAAGGAAACAGGACAGAAACCCACAAAGGTGG 581
Db 502 TATGCTTGTAGAGCTCACTCTGTCTAAGGAAACAGGCTGTGAAA--CACATGTGTGG 559
Qy 582 TAGAGAGAAATAGACAATAGACTGTGTAGAGGGAGTGAAGAGCCAGAGAGAGAA 641
Db 560 TAAAGAGAAAGAGACAAATAGATTGATGAAAGAGAGTGAAGTGTGCTTGTGCTG 619
Qy 642 ATGCTTACATCTGTGTAGAGAGTGTGTAAGAAAGATTAAATAGAAAGGGGTCTGTCTG 701
Db 620 ATGCTTACATCTGTGTAGAGAGTGTGTAAGAAAGATTAAAGAA--GGCTTGTCTG 678
Qy 702 GCTGGGCTTGCAGAGATGTGTAGAGATCTTAGGGGGCACAGTACCTTCAGGACAGAG 761
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Db 679 TCTGGGTTTGAAGAGATGTAGAGCTTCTAGGGGGCACAGGACACTCCAG----- 732
Qy 762 GAATTCATAGGTTAAAGATCTCAGTTGTGGCTTGTGGAGATGATTAAGTATTCG 821
Db 733 -----GCATAGTAAAGATCTGTAGGTGTGGCTTGTGGAGATGATTAAGTATTCG 786
Qy 822 GAATGAAGACGCCATGAAACAAAGGAGAGTGAAGAGATTTTAAGAGCTTCATGCCA 881
Db 787 GAATGAAGACGCCATGAAACAAAGGAGAGAGAGGCGATTTAAATGATTTTATGCCA 846
Qy 882 ATGGCTCCACTTGAATTTCTGATTAAGAACTCAGATTCGGTGAATCCCTGATTAATGA 941
Db 847 ATGGCTCCACTTGAATTTCTGATTAAGAACTCAGATTCGGTGAATCCCTGATTAATGA 906
Qy 942 TTAAGTTTATGATTTCCCATGATATGAACTCAAAAGAGGTAAAG--CAAGAGGTGT 1000
Db 907 TTGAGTTGTTATGATTAATCTCATTAAGATTAAGATCAAAAGAGGTGATGATGTGTGT 966
Qy 1001 GTGCGATTCTT----- 1011
Db 967 GTGCGATTCTTCCCAACTTCCAAAGGTGAAGAGCTCTTCCAACTGACAGGACAGCA 1026
Qy 1012 -----TGTACTGCTGACGTGACGCCCGCTCTTCCAGACATTAACATTT 1063
Db 1027 GTGGCCCTGCTACTGCTGCTGACGTGACCTGCTCTCTCTGATTAATTAACATTC 1086
Qy 1064 CACAGCTTGAACCTTAA--GACTGTGTGTCAGAGGAGGAGATCTCAGGACAGACGCCAGC 1122
Db 1087 CAACAGCTCACTGAATCACTGCTGTGACAGGACAGAAAGCTCATGATCACTAGCCAGC 1146
Qy 1123 AAACAACAGACACAGCTGAAAGTAAAGTCAAGAGAGACAGTGAAGAAAGCAAGTGGC 1182
Db 1147 AAAGAGCAACACAGAGCTGAAGAAAGTCAAGAGAGAGATTAAGTAAAGAAAGTGT 1206
Qy 1183 GATGACCTTATCCCAATTTGGCGGTGAAGACCTGCTCTCTGCTGTCAGCTGTGT 1242
Db 1207 GATGACCTTATCCCAAGCTTGGCCATGAAAGCTGCTCTCTGCTGTCAGCTGTGT 1266
Qy 1243 GCTCCTCTATCT 1254
Db 1267 GCTCCTCTATCT 1278
```

```
RESULT 5
US-10-085-612-3
; Sequence 3, Application US/10085612
; Publication No. US20030096251A1
; GENERAL INFORMATION:
; APPLICANT: Guido, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Vredenburg, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Markes, Jeffrey
; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
; FILE REFERENCE: 4389-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-085-612-3
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```
Query Match 39.8%; Score 498.8; DB 14; Length 1345;
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Best Local Similarity 77.7%; Pred. No. 8,4e-153; Matches 709; Conservative 1; Mismatches 128; Indels 74; Gaps 6;

QY 402 GGATGACACACAGAGGCCCCGACATCTCACCCAAAGTAACTCCACCAATTTCTGTCA 461
DB 382 GGATGACATAGCAAGGCCAGCAATCTCAGCTAACTCAACCCAGCTTTCTAGTTG 441
QY 462 CCCACCATGTGTACAGTACCTCTAGAGGTCCAGGGTCATGAAAGTAATATACAGAC 521
DB 442 CCCACTGTGTACAGACCTCTGTAGAGGCCAGAGCCATGACAGGAAATAGACTAGAC 501
QY 522 TGTGCCCCGAGGAACTCAGCTCTGTAGAGGAAACAGGACAGAAACCCAGAGGTGG 581
DB 502 TATGCCCTTGAGAGGCTCAGCTCTGTAGAGGAAACAGGAGTGGAA--CACATGTGG 559
QY 582 TAGAGAGAAATAGACATAGACCTGTGTAGAGGGAGATAGAGGCCACCCAGAGAGAA 641
DB 560 TAAAGAGAAAGAGCAATAGATGTCATGAAAGGGAGTGAAGTCCAGAGGAGAGAA 619
QY 642 ATGGTTACATCTGTGTAGAGAGGTGTGTAAGAAAGCTTTAATAGAAAGGGTCTGTG 701
DB 620 ATGGTTACATCTGTGTAGAGAGGTGTGTAGAGAAAGCTTTAGAGAA--GGCTCTGTG 678
QY 702 GCTGGGCTTGCAAGATGTGTAGAGGTCTATCTAGGGGGCAAAAGTACCTCAGGCAAG 761
DB 679 TCTGGGTTTGAAGAGATGTGTAGAGGTCTTCTAGGGGGCAAGGCACTCCAG----- 732
QY 762 GGAATTCATGTGGTAAAGATCTGAGTTGTGGGCTTGTGGGATGATTTCAATATCTG 821
DB 733 -----GCATAGGTAAAGATCTGTAGAGGTGTGGCTTGTGGAGTGAATTTCAAGATTTG 786
QY 822 GAATGAGAGAGCCATGAGAAACAGGCGAGGTGAGAGATATTAAAGGCTTCATGCCA 881
DB 787 GAATGAGAGAGCCATGAGAAACAGGCGAGGTGAGAGATATTAAAGGCTTCATGCCA 846
QY 882 ATGGCTCCACTTCACTTGTATAGAACTCAGGTTCCGTGACTCCGTATTAACCTGA 941
DB 847 ATGGCTCCACTTCACTTGTATAGAACTCAGGTTCCGTGACTCCGTATTAACCTGA 906
QY 942 TTAAGTTGTTATGATTTCCCATAGAAATATGAATCAAGAGAGTAAAG--CAAGGGGTGT 1000
DB 907 TTAAGTTGTTATGATTTCCCATAGAAATATGAATCAAGAGAGTCAAGTGTGTGTGT 966
QY 1001 GTGCGATTCTT----- 1011
DB 967 GTGCGATTCTTGTGCAACTTCCAAAGTGAAGAGCTTCTTCAACTGCAAGGCAAGACA 1026
QY 1012 -----TGTACTGGCTGAGCTGAGCCCGGCTCTTCTTCAGACATTAACATTT 1063
DB 1027 GTGGGCTTCTACTGTGCTGAGCTCAGGCTGCTGCTTCTTCTACATATTAACAATC 1086
QY 1064 CAGCAGCTTACCTAA--GACTGCTGTGCAAGGGCAGGAGTCTCAGGCAAGCCAGC 1122
DB 1087 CAGCAGCTTACCTAACTGCTGTGCAAGGGCAGGAGATCTCATCAATAGCCAGC 1146
QY 1123 AAACAACAGACACAGCTGAAGTAAGTAAGTCAAGGAGACAGTTGAAGAGGCAAGGTC 1182
DB 1147 AAAGAGACACAGAGCTGAAGTAAGTAAGTCAAGGAGAGAGTAAGTAAGAGAAAGT 1206
QY 1183 GATGACCTGATCCCAATTTGGCGGTGAGAACTGTGCTTCTCTGCTGTCAAGCTGT 1242
DB 1207 GATGACCTGATCCCAATTTGGCGGTGAGAACTGTGCTTCTCTGCTGTCAAGCTGT 1266
QY 1243 GCTCTCTATCT 1254
DB 1267 GCTCTCTATCT 1278

RESULT 6
US-09-943-115A-1
; Sequence 1, Application US/09943115A
; Publication No. US20030017469A1
; GENERAL INFORMATION:

APPLICANT: SEQUENOM, Inc.
APPLICANT: Rinsger, Carl
APPLICANT: Anderson, Maria
APPLICANT: Lewander, Tommy
APPLICANT: Olafsson, Erik
TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9
FILE REFERENCE: 52459-20021.00
CURRENT APPLICATION NUMBER: US/09/943,115A
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: UK 0021286.0
NUMBER OF SEQ ID NOS: 73
PRIORITY FILING DATE: 2000-08-30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1345
TYPE: DNA
ORGANISM: Homo sapiens
US-09-943-115A-1

Query Match 39.7%; Score 498.4; DB 10; Length 1345;
Best Local Similarity 77.6%; Pred. No. 1.1e-152; Matches 708; Conservative 2; Mismatches 128; Indels 74; Gaps 6;

QY 402 GGATGACACACAGAGGCCCCGACATCTCACCCAAAGTAACTCCACCAATTTCTGTCA 461
DB 382 GGATGACATAGCAAGGCCAGCAATCTCAGCTAACTCAACCCAGCTTTCTAGTTG 441
QY 462 CCCACCATGTGTACAGTACCTCTAGAGGTCCAGGGTCATGAAAGTAATATACAGAC 521
DB 442 CCCACTGTGTACAGACCTCTGTAGAGGTCTGTAGAGGCCAGAGCATGAGGAAATAGACTAGAC 501
QY 522 TGTGCCCCGAGGAACTCAGCTCTGTAGAGGAAACAGGACAGAAACCCAGAGGTGG 581
DB 502 TATGCCCTTGAGAGGCTCAGCTCTGTAGAGGAAACAGGAGTGGAA--CACATGTGG 559
QY 582 TAGAGAGAAATAGACATAGACCTGTGTAGAGGGAGATAGAGGCCACCCAGAGAGAA 641
DB 560 TAAAGAGAAAGAGCAATAGATGTCATGAAAGGGAGTGAAGTCCAGAGGAGAGAA 619
QY 642 ATGGTTACATCTGTGTAGAGAGGTGTGTAAGAAAGCTTTAATAGAAAGGGTCTGTG 701
DB 620 ATGGTTACATCTGTGTAGAGAGGTGTGTGAGAAAGCTTTAAGAGAA--GGCTCTGTG 678
QY 702 GCTGGGCTTGCAAGATGTGTAGAGGTCTATCTAGGGGGCAAAAGTACCTCAGGCAAG 761
DB 679 TCTGGGTTTGAAGAGATGTGTAGAGGTCTTCTAGGGGGCAAGGCACTCCAG----- 732
QY 762 GGAATTCATGTGGTAAAGATCTCAGTGTGCTTGTGGGATGATTTCAATATTTCTG 821
DB 733 -----GCATAGGTAAAGATCTGTAGAGGTGTGGCTTGTGGAGTGAATTTCAAGATTTG 786
QY 822 GAATGAGAGAGCCATGAGAAACAGGCGAGGTGAGAGATATTAAAGGCTTCATGCCA 881
DB 787 GAATGAGAGAGCCATGAGAAACAGGCGAGGTGAGAGATATTAAAGGCTTCATGCCA 846
QY 882 ATGGCTCCACTTCACTTGTATAGAACTCAGGTTCCGTGACTCCGTATTAACCTGA 941
DB 847 ATGGCTCCACTTCACTTGTATAGAACTCAGGTTCCGTGACTCCGTATTAACCTGA 906
QY 942 TTAAGTTGTTATGATTTCCCATAGAAATATGAATCAAGAGAGTAAAG--CAAGGGGTGT 1000
DB 907 TTAAGTTGTTATGATTTCCCATAGAAATATGAATCAAGAGAGTCAAGTGTGTGTGT 966
QY 1001 GTGCGATTCTT----- 1011
DB 967 GTGCGATTCTTGTGCAACTTCCAAAGTGAAGAGCTTCTTCAACTGCAAGGCAAGACA 1026
QY 1012 -----TGTACTGGCTGAGCTGAGCCCGGCTCTTCTTCAGACATTAACATTT 1063
DB 1027 GTGGGCTTCTACTGTGCTGAGCTCAGGCTGCTGCTTCTTCTACATATTAACAATC 1086
QY 1064 CAGCAGCTTACCTAA--GACTGCTGTGCAAGGGCAGGAGTCTCAGGCAAGCCAGC 1122

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Db 1087 CAACAGCTCACTGAATCAGCTGTGTGACGGCAGGAAGCTTCATGACATGACCCAGC 1146
Qy 1123 AACCAACAGCAGCTGAAAGTAAGTCAAGAGACAGTGTGAAGAAAGGCAAGTGGC 1182
Db 1147 AAGAGCAACACAGAGCTGAAAGAGACATCAGAGAGAGATTAATGAAGAAAGTAT 1206
Qy 1183 GATGACCTCATCCCAATTTGGCGGTGAACCTGCTTCTCTGCTGTCAAGCTTGGT 1242
Db 1207 GATGCTCTCATCCCAAGCTTGGCCATGAAACCTGCTTCTCTGCTGTCAAGCTTGGT 1266
Qy 1243 GCTCCTCTATCT 1254
Db 1267 GCTCCTCTATCT 1278
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RESULT 7

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US-10-121-960C-14
; Sequence 14, Application US/10121960C
; Publication No. US20030145341A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, Weisheng
; APPLICANT: CONTAG, Pamela
; APPLICANT: PURCHIO, Anthony
; APPLICANT: HASHIMA, Sandy
; APPLICANT: MA, Shirley
; APPLICANT: NAMOTKA, Kevin
; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
; TITLE OF INVENTION: TRANSCRIPTION CONTROL ELEMENTS ASSOCIATED WITH
; TITLE OF INVENTION: CYTOCHROME EXPRESSION
; FILE REFERENCE: 9400-0014 / PXE-014.US
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 13035
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human CYP3A4 gene locus
US-10-121-960C-14
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Query Match 36.5%; Score 457.2; DB 15; Length 13035;
Best Local Similarity 77.1%; Pred. No. 1.6e-138;
Matches 665; Conservative 0; Mismatches 123; Indels 74; Gaps 6;

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Qy 384 TCACCAAGACTGAGAGGATGACACAGGGGCCCAAGAAATTCACCCAAATCACTC 443
Db 12189 TCACCAAGAAAGTCAGAGGATGACATGACAGAGGCCCAAGAAATTCAGTCACTC 12248
Qy 444 CACCAATTTCTGTCACCCACCATGTGTACAGTACCTGCTAGGGTCCAGGGTCACTGA 503
Db 12249 CACCAAGCTTTTCTGTCACCCACCATGTGTGTACAGTACCTGCTAGGGTCCAGGGTCACTGA 12308
Qy 504 AAGTAAATTAATCAGACTGTGCTTGTAGGAATCACTTCTGTAGAGGAAACAGGCAC 563
Db 12309 CAGGAAATTAAGACTAGACTATGCTTGTAGAGGACTCACTTCTGTAGAGGAAACAGGCCT 12368
Qy 564 AGAAACCCAGAGGATGTGAGAGGAAATGAGCAATTAAGACTGTGTAGAGGGAATGG 623
Db 12369 GGAAG--CACAATGTGTGTAAAGAGGAAAGCAATTAAGATTCAGAGGGGATGGA 12426
Qy 624 AGGACCCAGAGGAAATGTATCATCTGTGTAGAGGATGTGTAGAGAAAGACTTTTA 683
Db 12427 AGGTGCCAGAGGAGAAATGTGTATCATCTGTGTAGAGGATGTGTAGAGAAAGACTTTTA 12486
Qy 684 ATAGAGAGGGTGTGTGCTGTGCTGAGCTTGAAGATGTGTAGAGTCACTTAAGGGGACA 743
Db 12487 AGAGAA--GGCTGTGTGTGTGCTGAGGTTGAAGATGTGTAGAGTCTTTTAAGGGGACA 12545
Qy 744 AGTACATTCAGAGGAGGAATTCATGGGTAAAGATTCAGATTTGTGGCTTGTGGGA 803
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Db 12546 GGCACTCCAG-----GCATAGGTAAAGATCTGTAGGTGTGCTTTGGGA 12593
Qy 804 TGGATTTCAAGTATTTCTGAAATGAAGACAGCCATGGAACAAGGGCAGGTAGAGATAT 863
Db 12594 TGAATTTCAAGTATTTTGGAAATGAGGACAGCCATGAGACAAAGGGCAGAGGGGAT 12653
Qy 864 TTAAAGGCTTCAATGCCAATGGCTCCACATTTCTGATTAAGAACTCAGGTTCCGTGG 923
Db 12654 TTATATGATTTTATGCAATGGCTCCACATTTCTGATTAAGAACTCAGGTTCCGTGG 12713
Qy 924 ACTCCGATTAAGATGATTAAGTGTATGATTCGCCATAGAAATTAAGTCAAGAGA 983
Db 12714 ACTCCGATTAAGATGATTAAGTGTATGATTCGCCATAGAAATTAAGTCAAGAGA 12773
Qy 984 GGTAG--CAAGGGGTGTGTGCGATTT----- 1011
Db 12774 GGTAGTGAATGTGTGTGTGTATTTCTTGCCAACTTCCAGGTGAGAAAGCTTTCC 12833
Qy 1012 -----TGCTACTGGCTGACGCTGACGCTCCGCTTCC 1045
Db 12834 AACTGACGACAGACAGAGTGGCCCTGCTACTGCTGACGCTCCAGCTTCCCTTCC 12893
Qy 1046 TCCAGCAGATTAACATTTGACAGCTTGACCTAA--GACTGCTGACAGGCGAGGATGCT 1104
Db 12894 TCTAGCATTAATTAACATTCACAGCTTCACTGATTAATCACTGTGTGACAGGCAAGGAT 12953
Qy 1105 CCAAGCAGACAGCCCAAGCAACACAGCAGCTGAAATGAAGTCAAGAGAGACAG 1164
Db 12954 CCAATGACATTAAGCCCAAGCAACACAGAGCTGAAAGAAAGTCAAGAGAGAGAG 13013
Qy 1165 TTGAAGAGGCAAGTGGCATG 1186
Db 13014 ATAAAGTAAAGAAATGATGATG 13035
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RESULT 8

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US-10-121-960C-17
; Sequence 17, Application US/10121960C
; Publication No. US20030145341A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, Weisheng
; APPLICANT: CONTAG, Pamela
; APPLICANT: PURCHIO, Anthony
; APPLICANT: HASHIMA, Sandy
; APPLICANT: MA, Shirley
; APPLICANT: NAMOTKA, Kevin
; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
; TITLE OF INVENTION: TRANSCRIPTION CONTROL ELEMENTS ASSOCIATED WITH
; TITLE OF INVENTION: CYTOCHROME EXPRESSION
; FILE REFERENCE: 9400-0014 / PXE-014.US
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 15185
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CYP3A4-luc transgene
US-10-121-960C-17
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Query Match 34.7%; Score 434.6; DB 15; Length 15185;
Best Local Similarity 76.1%; Pred. No. 4.9e-131;
Matches 646; Conservative 0; Mismatches 129; Indels 74; Gaps 6;

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Qy 384 TCACCAAGACTGAGAGGATGACACAGGGGCCCAAGAAATTCACCCAAATCACTC 443
Db 12189 TCACCAAGAAAGTCAGAGGATGACATGACAGAGGCCCAAGAAATTCAGTCACTC 12248
Qy 444 CACCAATTTCTGTCACCCACCATGTGTACAGTACCTGCTAGGGTCCAGGGTCACTGA 503
Db 12249 CACCAAGCTTTTCTGTCACCCACCATGTGTGTACAGTACCTGCTAGGGTCCAGGGTCACTGA 12308
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QY	504	AACTAATATATATACAGACTGTGCCCTTGAGAACTACCTCTGCTAAAGGAAACAGGCAC	563
Db	12309	CAGGAAATTAAGACTAGACTATGCCCTTGAGACTCACTCTGTTCAAGGAAACAGCCGT	12366
QY	564	AGAAACCCACAAGGGTGTGAGAGAGAAATAGACAATAGACCTGTGTAGGGGATAGG	623
Db	12369	GGAAA--CAATAAGTGTGTAAAGAAAGAAAGACAATAGATATGCATTAAGGGGATAGGA	12428
QY	624	AGGCACCCNAGAGAGAAAATGTGTACATCTGTGTGAGAGGTGTGTAAAGAAAGACTTTA	683
Db	12427	AGGTGCCNAGGGAGGAAATGTGTACATCTGTGTGAGAGGTTGTGTAGAAAAGACTTTA	12486
QY	684	ATAGAAAGGGTCTGTCTGCGCTGGCTTGCAAGATGTGTAGAGTCACTAAGGGGACACA	743
Db	12487	AGAGAA--GGCTCTGTCTGTCTGTGGGTTTGAAAGATGTGTAGAGTCTTCTAAGGGGACACA	12545
QY	744	AGTACACTCCAGGCACAGGGAATTCGATGGGTAAAGATTCGACGTTGTGTGGTGGGA	803
Db	12546	GGCACACTCCAG-----GCATAGTGTAAAGTCTGTGTGGTGTGGCTGTTGGGA	12593
QY	804	TGCATTTCAAGTATTTCTGGAATGTAAAGACGCCATGTGAACCAAGGCAGGTGAGAGATAT	863
Db	12594	TGAATTTCAAGTATTTTGGAAATGAGACAGCCATTAAGACAAAGGCAAGAGAGAGGCAT	12653
QY	864	TTAAGAGGCTTCATATGCCAATGGCTCCCACTTCAGTTTCTGATTAAGACTAGGTTCCGTGG	923
Db	12654	TTAATATAGATTTTATATGCCAAATGGCTCCCACTTCAGTTTCTGATTAAGAACCCAGAACCTTTGG	12713
QY	924	ACTCCCTGATTAACCTGATTAAGTGTGTTATGAATTCCTCCATAGAAATATGAATCTCAAAAGA	983
Db	12714	ACTCCCAATGACATGTAATGAAGTGTGTTATGATTAATCTCATAGAAATATGAATCTCAAAAGA	12773
QY	984	GGTAAAG--CAAAAGGGGTGTGTGCATTTCTT-----	1011
Db	12774	GGTCAGTAGAGTGTGTGTGTGATTTCTTTTGCCAACTTCCAAAGTGAAGAGCTTTCC	12833
QY	1012	-----TGCTACTGTGCTGACGTGACGCCCGGCTCTTCC	1045
Db	12834	AACTGACAGGAGACAGACAGGTGGCCCTGTCTACTGTGGCTGTGACGTCTCAGCCCTGTCTTTC	12893
QY	1046	TCCAGCACAATTAACATTTTCAGACGCTTGACCTTA--GACTGTCTGTGACGGGACGAGATGCT	1104
Db	12894	TCTAGCATATTAACATTAACATTCACAGCCCTCACTGAATCACTGTCTGTGACGGGACGAGAAAGCT	12953
QY	1105	CCAGGCGAGACGCCCGACGAAACACACAGACACAGCTGAAAGTAAAGACTCAGAGGAAGACAG	1164
Db	12954	CCATGCGACATAGGCCCGACGAAAGAGCAACACAGAGCTGAAAGGAAGCTTGTGGCCGCTTTAA	13013
QY	1165	TTGAGAGG 1173	
Db	13014	CTGCAGAGG 13022	

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US RESULT 9
: Sequence 1, Application US/09957997
: Patent No. US20020150915A1
: GENERAL INFORMATION:
: APPLICANT: Berkenstam, Anders
: APPLICANT: Bertilsson, Gran
: APPLICANT: Blomquist, Patrik
: TITLE OF INVENTION: PROMOTER SEQUENCES
: FILE REFERENCE: 13425-046001
: CURRENT APPLICATION NUMBER: US/09/957,997
: CURRENT FILING DATE: 2001-09-21
: EARLIER APPLICATION NUMBER: SE 0003393-6
: EARLIER FILING DATE: 2000-09-22
: EARLIER APPLICATION NUMBER: 60/238,895
: EARLIER FILING DATE: 2000-10-10
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1

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[illegible]

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: APPLICANT: Blomquist, Patrik
: TITLE OF INVENTION: PROMOTER SEQUENCES
: FILE REFERENCE: 13425-046001
: CURRENT APPLICATION NUMBER: US/09/957,997
: CURRENT FILING DATE: 2001-09-21
: EARLIER APPLICATION NUMBER: SE 0003393-6
: EARLIER FILING DATE: 2000-09-22
: EARLIER APPLICATION NUMBER: 60/738,895
: EARLIER FILING DATE: 2000-10-10
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 1012
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-957-997-4

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Best Local Similarity	93.7%;	Pred. No. 3.8e-35;	
Matches	148;	Conservative	0; Mismatches 10; Indels 0; Gaps 0;
QY	1097	GGGATGCTCCAGGCGAGACAGCCCAAGCAAAACAAGCACACAGCTGAAAGTAAAGCTCAGA	1156
Db	1	GGGAAGCTCCAGGCAAAACAGCCCAAGCAAAACAGACGACTCAGCTTAAAGAAAGACTCA	60
QY	1157	GGAGACAGTTAAGAGGCGAAGTGGCGATGACCTCATCCCAAAATTGGCGGTGAAAAC	1216
Db	61	GAACACAGTTAAAGAAAGAAAGTGGCGATGACCTCATCCCAAAATTGGCGGTGAAAAC	120
QY	1217	TGGCTTCTCTGGCTGTGACGCTGGTGTCTCTATCT	1254
Db	121	TGGCTTCTCTGGCTGTGACGCTGGTGTCTCTATCT	158

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      RESULT 14
      US-10-641-643-1060
      : Sequence 1060, Application US/10641643
      : Publication No. US20040077003A1
      :
      : GENERAL INFORMATION:
      :   APPLICANT: Cocks, Benjamin G.
      :             Susan G. Stuart
      :             Jeffrey J. Sellhammer
      :
      : TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
      :                       GENE EXPRESSION
      :
      : NUMBER OF SEQUENCES: 1508
      :
      : CORRESPONDENCE ADDRESSES:
      :   ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
      :   STREET: 3174 PORTER DRIVE
      :   CITY: PALO ALTO
      :   STATE: CALIFORNIA
      :   COUNTRY: USA
      :   ZIP: 94304
      :
      : COMPUTER READABLE FORM:
      :   MEDIUM TYPE: Floppy disk
      :   COMPUTER: IBM PC compatible
      :   OPERATING SYSTEM: PC-DOS/MS-DOS
      :   SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
      :
      : CURRENT APPLICATION DATA:
      :   APPLICATION NUMBER: US/10/641,643
      :   FILING DATE: 14-Aug-2003
      :   CLASSIFICATION: <Unknown>
      :
      : PRIOR APPLICATION DATA:
      :   APPLICATION NUMBER: <Unknown>
      :   FILING DATE: <Unknown>
      :
      : ATTORNEY/AGENT INFORMATION:
      :   NAME: Zeller, Karen J.
      :   REGISTRATION NUMBER: 37,071
      :
      : REFERENCE/DOCKET INFORMATION:
      :   TELECOMMUNICATION INFORMATION:
      :     TELEPHONE: (650) 855-0555
      :     TELEFAX: (650) 845-4166
      :
      : INFORMATION FOR SEQ ID NO: 1060:
      :   SEQUENCE CHARACTERISTICS:
      :     LENGTH: 1707 base pairs
      :     TYPE: nucleic acid
      :     STRANDEDNESS: single
      :     TOPOLOGY: linear
      :
      :   IMMEDIATE SOURCE:
      :     LIBRARY: GENBANK
      :     CLONE: g181345
      :
      : SEQUENCE DESCRIPTION: SEQ ID NO: 1060 :
      :
      : US-10-641-643-1060
    
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Query Match	11.3%	Score 142;	DB 16;	Length 1707;
Best Local Similarity	93.7%	Pred. No. 3.8e-35;		
Matches 148;	Conservative 0;	Mismatches 10;	Indels 0;	Gaps 0;
OY	1097	GGGATGCTCCAGGCGAGACGCCCTCCGAAACACAGCACACAGCTGAAGTAACTCAGCA	1156	
Db	1	GGGAAAGCTCCAGGCGAAACAGCCCTCCGAAACACAGCACACTCAGTAAAGGAAGCTCACA	60	

QY	1157	GGAAACAGTTGAAAGAAAGGCAAGTGCGCATGGACCTCAATCCCAAAATTGGCGCGTGGAAAC	1216
Db	61	GAAACACAGTTGAAAGAAAGGAAAGTGCGCATGGACCTCAATCCCAAAATTGGCGCGTGGAAAC	120
QY	1217	TGGCTTCTCCGCGCTGTCAGCTGCGTGTCTCTATAT	1254
Db	121	TGGCTTCTCTCGCTGCTGTCAGCTGCTGTCTCTATCT	158

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RESULT 15
US-09-925-297-24
: Sequence 24, Application US/09925297
: Patent No. US20020081659A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
: FILE REFERENCE: PA105
: CURRENT APPLICATION NUMBER: US/09/925,297
: CURRENT FILING DATE: 2001-08-10
: PRIOR APPLICATION NUMBER: PCT/US00/05989
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: 60/124,270
: PRIOR FILING DATE: 1999-03-12
: NUMBER OF SEQ ID NOS: 928
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 24
: LENGTH: 384
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (357)
: OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-24

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Query Match	11.2%;	Score 141;	DB 9;	Length 384;
Best Local Similarity	93.6%;	Pred. No. 3.4e-35;		
Matches 147;	Conservative	0;	Mismatches 10;	Indels 0;
				Gaps 0;

Oy	1158	GAGCAGTTGAAAGGCAAGTGGCAGTGAACCTCATCCAAATTGGCGGTGAAACT	1217
Db	61	AACACAGTTGAAAGGAAAGTGGCGATGACCTCATCCCAAAATTGGCGGTGAAACT	120
Oy	1218	GGCTTCTCCTGGCTCTGACCTGGTGGTCCCTCAATCT	1254
Db	121	GGCTTCTCCTGGCTGTGACCTGGAGTCTCCCTCAATCT	157

Search completed: January 26, 2005, 19:49:30
Job time : 635.441 secs

seq4-1010-1060-1037g.rn1

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 13:23:32 ; Search time 4.22069 Seconds
(without alignments)
8588.699 Million cell updates/sec

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Title:      SEQ4-1010-1060-1037G
Perfect score: 51
Sequence:  1 ttgtctactgctgcagctg.....ccttcgcagacataaaca 51
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 1649014

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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2 : /cgn2_6/prodata/1/ina/5B.COMB.seq:*
3 : /cgn2_6/prodata/1/ina/6A.COMB.seq:*
4 : /cgn2_6/prodata/1/ina/6B.COMB.seq:*
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6 : /cgn2_6/prodata/1/ina/bkaffile.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	39.4	77.3	1345	3	US-09-312-339-1	Sequence 1, Appl1
2	39.4	77.3	1345	3	US-09-312-339-2	Sequence 2, Appl1
3	39.4	77.3	1345	3	US-09-144-367-3	Sequence 3, Appl1
4	27	52.9	873	4	US-09-282-991A-5146	Sequence 5146, Appl1
5	27	52.9	981	4	US-09-282-991A-5003	Sequence 5003, Appl1
6	27	52.9	1581	4	US-09-282-991A-5177	Sequence 5177, Appl1
7	26.2	51.4	320	4	US-09-513-999C-33490	Sequence 33490, Appl1
8	26.2	51.4	1578	4	US-09-252-991A-5039	Sequence 5039, Appl1
9	25.4	49.8	2292	4	US-09-270-767-15045	Sequence 15045, Appl1
10	25.2	49.4	927	4	US-09-248-796A-246	Sequence 246, Appl1
11	25	49.0	6674	4	US-09-620-312D-110	Sequence 110, Appl1
12	24.8	48.6	1588	4	US-09-450-221-7	Sequence 7, Appl1
13	24.8	48.6	2338	1	US-08-435-069-1	Sequence 1, Appl1
14	24.8	48.6	2338	2	US-08-317-844B-1	Sequence 1, Appl1
15	24.8	48.6	3245	4	US-09-270-767-13706	Sequence 13706, Appl1
16	24.4	47.8	445	4	US-09-270-767-6152	Sequence 6152, Appl1
17	24.4	47.8	445	4	US-09-270-767-21434	Sequence 21434, Appl1
18	24.4	47.8	3028	4	US-09-352-916-2	Sequence 2, Appl1
19	24.2	47.5	795	4	US-09-795-926-47	Sequence 47, Appl1
20	24.2	47.5	4182	1	US-07-973-357-1	Sequence 1, Appl1
21	24	47.1	2190	4	US-09-270-767-26507	Sequence 26507, Appl1
22	24	47.1	2366	4	US-09-799-451-551	Sequence 351, Appl1
23	24	47.1	2760	4	US-09-270-767-13149	Sequence 13149, Appl1
24	24	47.1	2913	4	US-09-270-767-11002	Sequence 11002, Appl1
25	23.8	46.7	511	4	US-09-556-877-271	Sequence 271, Appl1
26	23.8	46.7	511	4	US-09-620-412C-271	Sequence 271, Appl1
27	23.8	46.7	511	4	US-09-558-419-271	Sequence 271, Appl1

28	23.8	46.7	831	4	US-09-252-991A-5118	Sequence 5118, App
29	23.8	46.7	1965	4	US-09-020-412C-340	Sequence 340, App
30	23.8	46.7	1965	4	US-09-598-413-340	Sequence 340, App
31	23.8	46.7	1965	4	US-09-598-413-340	Sequence 340, App
32	23.8	46.7	1965	4	US-09-598-413-340	Sequence 340, App
33	23.8	46.7	1965	4	US-09-598-413-340	Sequence 340, App
34	23.8	46.7	1965	4	US-09-598-413-340	Sequence 340, App
35	23.8	46.7	1965	4	US-09-598-413-340	Sequence 340, App
36	23.8	46.7	1965	4	US-09-598-413-340	Sequence 340, App
37	23.8	46.7	1965	4	US-09-598-413-340	Sequence 340, App
38	23.8	46.7	1965	4	US-09-598-413-340	Sequence 340, App
39	23.8	46.7	1965	4	US-09-598-413-340	Sequence 340, App
40	23.8	46.7	1965	4	US-09-598-413-340	Sequence 340, App
41	23.8	46.7	1965	4	US-09-598-413-340	Sequence 340, App
42	23.8	46.7	1965	4	US-09-598-413-340	Sequence 340, App
43	23.8	46.7	1965	4	US-09-598-413-340	Sequence 340, App
44	23.8	46.7	1965	4	US-09-598-413-340	Sequence 340, App
45	23.8	46.7	1965	4	US-09-598-413-340	Sequence 340, App

ALIGNMENTS

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RESULT 1
US-09-372-339-1
: Sequence 1, Application US/09372339
: Patent No. 6174684
: GENERAL INFORMATION:
: APPLICANT: Rebbeck, Timothy
: APPLICANT: Felix, Carolyn
: TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
: FILE REFERENCE: PENN-0695
: CURRENT APPLICATION NUMBER: US/09/372.339
: CURRENT FILING DATE: 1999-08-11
: EARLIER APPLICATION NUMBER: 60/096,586
: EARLIER FILING DATE: 1998-08-14
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 1345
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-372-339-1

Query Match          77.3%; Score 39.4; DB 3; Length 1345;
Best Local Similarity 87.8%; Pred. No. 0.00033;
Matches 43; Conservative 0; Mismatches 6; Indels 0; Gaps 0

Qy          3 TGGTACTGCTGCAGCTGCAGACCCCACTCTTCTGCAGCATATAACA 51
            |||||
Db          1035 TGGTACTGCTGCAGCTGCAGACCCCTGCTCTTCTGCAGCATATAACA 1083

RESULT 2
US-09-372-339-2
: Sequence 2, Application US/09372339
: Patent No. 6174684
: GENERAL INFORMATION:
: APPLICANT: Rebbeck, Timothy
: APPLICANT: Felix, Carolyn
: TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
: FILE REFERENCE: PENN-0695
: CURRENT APPLICATION NUMBER: US/09/372.339
: CURRENT FILING DATE: 1999-08-11
: EARLIER APPLICATION NUMBER: 60/096,586
: EARLIER FILING DATE: 1998-08-14
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 1345
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-372-339-2

```

Query Match 77.3%; Score 39.4; DB 3; Length 1345;
Best Local Similarity 87.8%; Pred. No. 0.00039;
Matches 43; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TGCTACTGGCTGCGAGTGCAGCCCACTCTTCTGCAGCACAATAACA 51
Db 1035 TGCTACTGGCTGCGAGTGCAGCCCTGCTCTTCTGCAGCACAATAACA 1083

RESULT 3

US-09-144-367-3
; Sequence 3, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Licher, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0)...(0)
US-09-144-367-3

Query Match 77.3%; Score 39.4; DB 4; Length 1345;
Best Local Similarity 87.8%; Pred. No. 0.00039;
Matches 43; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TGCTACTGGCTGCGAGTGCAGCCCACTCTTCTGCAGCACAATAACA 51
Db 1035 TGCTACTGGCTGCGAGTGCAGCCCTGCTCTTCTGCAGCACAATAACA 1083

RESULT 4

US-09-252-991A-5146/C
; Sequence 5146, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5146
; LENGTH: 873
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5146

Query Match 52.9%; Score 27; DB 4; Length 873;
Best Local Similarity 70.6%; Pred. No. 4.4;
Matches 36; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TTTGCTACTGGCTGCGAGTGCAGCCCACTCTTCTGCAGCACAATAACA 51
Db 70 TTGCTCATGCTGCGAGTGCAGCCGCGACCTGCGCCCGCAGCAGTAGCCA 20

RESULT 5
US-09-252-991A-5003
; Sequence 5003, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5003
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5003

Query Match 52.9%; Score 27; DB 4; Length 981;
Best Local Similarity 70.6%; Pred. No. 4.5;
Matches 36; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TTTGCTACTGGCTGCGAGTGCAGCCCACTCTTCTGCAGCACAATAACA 51
Db 140 TTGCTCATGCTGCGAGTGCAGCCGCGACCTGCGCCCGCAGCAGTAGCCA 190

RESULT 6

US-09-252-991A-5177/C
; Sequence 5177, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5177
; LENGTH: 1581
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5177

Query Match 52.9%; Score 27; DB 4; Length 1581;
Best Local Similarity 70.6%; Pred. No. 5.1;
Matches 36; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TTTGCTACTGGCTGCGAGTGCAGCCCACTCTTCTGCAGCACAATAACA 51
Db 141 TTGCTCATGCTGCGAGTGCAGCCGCGACCTGCGCCCGCAGCAGTAGCCA 91

RESULT 7

US-09-513-999C-33490/C
; Sequence 33490, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961

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FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513.999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 33490
LENGTH: 320
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2
OTHER INFORMATION: r=a or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: 12
OTHER INFORMATION: r=a or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: 14
OTHER INFORMATION: r=a or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: 205
OTHER INFORMATION: r=a or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: 171
OTHER INFORMATION: s=g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: 282
OTHER INFORMATION: w=a or t
US-09-513.999C-33490

Query Match 51.4%; Score 26.2; DB 4; Length 320;
Best Local Similarity 69.4%; Pred. No. 6.4;
Matches 34; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

QY 2 TTGCTACTGGCTGCGAGCTGCGAGCCCACTCTCTTCTGACAGACATAAC 50
DB 173 TCGCCGCTCACCGAGAGAGAGAGACCACTCTGACAGACAGAGAC 125

RESULT 8
US-09-252-991A-5039
Sequence 5039, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 5039
LENGTH: 1578
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5039

Query Match 51.4%; Score 26.2; DB 4; Length 1578;
Best Local Similarity 72.3%; Pred. No. 9.3;
Matches 34; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 TTGCTACTGGCTGCGAGCTGCGAGCCCACTCTTCTGACAGACATA 47
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DB 1531 TTGCTACTGGCTGCGAGCTGCGAGCCCACTCTGACAGACATA 1577

RESULT 9
US-09-270-767-15045/C
Sequence 15045, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270.767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 15045
LENGTH: 2292
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-15045

Query Match 49.8%; Score 25.4; DB 4; Length 2292;
Best Local Similarity 68.6%; Pred. No. 19;
Matches 35; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 TTGCTACTGGCTGCGAGCTGCGAGCCCACTCTTCTGACAGACATA 51
DB 240 TTGATTTGGCTCTGCTGCTCCAGCTCCAGCTCCAGCTGAGCTGCGCA 190

RESULT 10
US-09-248-796A-246
Sequence 246, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248.796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 246
LENGTH: 927
TYPE: DNA
ORGANISM: Candida albicans
US-09-248-796A-246

Query Match 49.4%; Score 25.2; DB 4; Length 927;
Best Local Similarity 71.7%; Pred. No. 18;
Matches 33; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 3 TGGTACTGGCTGCGAGCTGCGAGCCCACTCTTCTGACAGACATA 48
DB 749 TGGCAGCGCCAGCAGCTCCAGCTCTGCTGCGCCCAATAA 794

RESULT 11
US-09-620-312D-110
Sequence 110, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
```


US-08-317-844B-1/c
Sequence 1, Application US/08317844B
Patent No. 5989894
GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Xu, Ming
APPLICANT: Himmann, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5989894th Washington Street
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22046
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,844B
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-105P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
TELEFAX: (703) 241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Nephilia clavipes
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2154
OTHER INFORMATION: /product= "Nephilia clavipes"
OTHER INFORMATION: dragline silk protein"
PUBLICATION INFORMATION:
AUTHORS: Xu, Ming
AUTHORS: Lewis, Randolph V.
TITLE: Structure of a protein superfiber: Spider
TITLE: dragline silk
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 87
PAGES: 7120-7124
DATE: Sept.-1990
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 2338
US-08-317-844B-1

Query Match 48.6%; Score 24.8; DB 2; Length 2338;
Best Local Similarity 80.6%; Pred. No. 30;
Matches 29; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 11 GCTGACGTGAGCGCCGACCTCTCTGACGACAT 46
DB 1697 GCTGACGTGAGCGCTCTGACGCTCTGACGACAT 1662

RESULT 15
US-09-270-767-13706

Sequence 13706, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13706
LENGTH: 3246
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-13706

Query Match 48.6%; Score 24.8; DB 4; Length 3246;
Best Local Similarity 72.7%; Pred. No. 32;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 3 TGCTACTGCTGAGCGCGACCGCCGACCTCTCTGACGACAT 46
DB 306 TGATATTGCGAGCTGCGAGCGCGCACTCTCTCTCATCTCT 349

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Job time : 9.22069 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 17:54:48 ; Search time 25.5586 Seconds
(without alignments)
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Title: SEQ4-1010-1060-1037G

Perfect score: 51
Sequence: 1 ttctgcctacgtgcctgcagctg.....cctctgcagcacaataaca 51

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCRTUS_PUBCOMB.seq:*
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- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49.4	96.9	1254	14	US-10-085-612-4
2	41	80.4	1012	9	US-09-957-997-4
3	41	80.4	1186	9	US-09-957-997-1
4	39.4	77.3	1345	10	US-09-943-115A-1
5	39.4	77.3	1345	14	US-10-146-575-3
6	39.4	77.3	1345	14	US-10-085-612-3
7	39.4	77.3	13035	15	US-10-121-960C-14
8	39.4	77.3	15185	15	US-10-121-960C-17
9	31.4	61.6	8943	16	US-10-257-166-48
10	29.8	58.4	8776	16	US-10-257-166-150
11	28	54.9	34	14	US-10-085-612-6
12	27.2	53.3	4130	17	US-10-775-169-80

13	27.2	53.3	8575	10	US-09-764-891-8707	Sequence 8707, Ap
14	27	52.9	34	14	US-10-085-612-2	Sequence 2, Appl
15	26.6	52.2	704	18	US-10-425-115-176951	Sequence 176951
16	25.8	50.6	12614	15	US-10-242-355-1086	Sequence 1086, Ap
17	25.8	50.6	22314	17	US-10-322-281-164	Sequence 164, App
18	25.6	50.2	306	17	US-10-437-963-70996	Sequence 70996, A
19	25.6	50.2	384	16	US-10-424-599-115210	Sequence 115210,
20	25.6	50.2	493	11	US-09-732-627A-2583	Sequence 2583, Ap
21	25.6	50.2	572	13	US-10-027-633-196479	Sequence 196479,
22	25.6	50.2	572	15	US-10-027-632-196479	Sequence 196479,
23	25.6	50.2	1158	15	US-10-369-493-36839	Sequence 36839, A
24	25.6	50.2	3015	16	US-10-263-923-43	Sequence 43, Appl
25	25.4	49.8	259	10	US-09-764-891-7918	Sequence 7918, Ap
26	25.4	49.8	627	9	US-09-770-149-726	Sequence 726, App
27	25.4	49.8	5541	10	US-09-930-213-272	Sequence 272, App
28	25.4	49.8	5541	15	US-10-341-434-74	Sequence 74, Appl
29	25.4	49.8	5541	18	US-10-622-377-9	Sequence 9, Appl
30	25.4	49.8	5612	16	US-10-276-774-846	Sequence 846, App
31	25.4	49.8	31364	17	US-10-741-601-5672	Sequence 5672, Ap
32	25.4	49.8	53331	17	US-10-741-601-5762	Sequence 5762, Ap
33	25.2	49.4	160	16	US-10-424-599-83796	Sequence 83796, A
34	25	49.0	402	10	US-09-764-891-2198	Sequence 2198, Ap
35	25	49.0	871	13	US-10-027-632-166228	Sequence 166228,
36	25	49.0	871	15	US-10-027-632-166228	Sequence 166228,
37	25	49.0	5010	10	US-09-918-715-251	Sequence 251, App
38	25	49.0	5010	15	US-10-172-118-680	Sequence 680, App
39	25	49.0	5010	16	US-10-342-887-680	Sequence 680, App
40	25	49.0	5010	18	US-10-474-794-251	Sequence 251, App
41	25	49.0	5662	15	US-10-084-817-91	Sequence 91, Appl
42	25	49.0	6021	10	US-09-814-352-20075	Sequence 20075, A
43	25	49.0	6021	14	US-10-198-846-10879	Sequence 10879, A
44	25	49.0	6447	16	US-10-159-563-133	Sequence 133, App
45	25	49.0	6674	15	US-10-037-270-110	Sequence 110, App

ALIGNMENTS

RESULT 1
US-10-085-612-4
Sequence 4, Application US/10085612
Publication No. US20030096251A1
GENERAL INFORMATION:
APPLICANT: Guida, Marco
APPLICANT: Hall, Jeff
APPLICANT: Petros, William
APPLICANT: Vredenburg, James
APPLICANT: Colvin, Oliver
APPLICANT: Marks, Jeffrey
TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
FILE REFERENCE: 4389-5-Cl
CURRENT APPLICATION NUMBER: US/10/085,612
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/144,367
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/271,630
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 1254
TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-612-4
Query Match: 96.9%; Score 49.4; DB 14; Length 1254;
Best Local Similarity 98.0%; Pred. No. 3.1e-07;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 1010 TTGCTACTGGCTGCAGCTGCAGCCCACTCTTCTGCAGCATTAACA 51
1010 TTGCTACTGGCTGCAGCTGCAGCCCACTCTTCTGCAGCATTAACA 1060

RESULT 2
US-09-957-997-4
; Sequence 4, Application US/09957997
; Patent No. US20020150915A1
; GENERAL INFORMATION:
; APPLICANT: Berkenstam, Anders
; APPLICANT: Blomquist, Patrik
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-046001
; CURRENT APPLICATION NUMBER: US/09/957,997
; CURRENT FILING DATE: 2001-09-21
; EARLIER APPLICATION NUMBER: SE 0003393-6
; EARLIER FILING DATE: 2000-09-22
; EARLIER APPLICATION NUMBER: 60/238,895
; EARLIER FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1012
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-957-997-4

Query Match 80.4%; Score 41; DB 9; Length 1012;
Best Local Similarity 89.8%; Pred. No. 0.00022;
Matches 44; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 TGCTACTGGCTGCGAGCTGCAGCCCACTCTTCTTGACGACATTAACA 51
Db 947 TGCTACTGGCTGCGAGCTGCAGCCCTGCTCTCTCCAGCATTAACA 995

RESULT 3
US-09-957-997-1
; Sequence 1, Application US/09957997
; Patent No. US20020150915A1
; GENERAL INFORMATION:
; APPLICANT: Berkenstam, Anders
; APPLICANT: Blomquist, Patrik
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-046001
; CURRENT APPLICATION NUMBER: US/09/957,997
; CURRENT FILING DATE: 2001-09-21
; EARLIER APPLICATION NUMBER: SE 0003393-6
; EARLIER FILING DATE: 2000-09-22
; EARLIER APPLICATION NUMBER: 60/238,895
; EARLIER FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1186
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-957-997-1

Query Match 80.4%; Score 41; DB 9; Length 1186;
Best Local Similarity 89.8%; Pred. No. 0.00027;
Matches 44; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 TGCTACTGGCTGCGAGCTGCAGCCCACTCTTCTTGACGACATTAACA 51
Db 11064 TGCTACTGGCTGCGAGCTGCAGCCCTGCTCTCTCCAGCATTAACA 11112

RESULT 4
US-09-943-115A-1
; Sequence 1, Application US/09943115A
; Publication No. US20030017469A1
; GENERAL INFORMATION:

APPLICANT: SEQUENOM, Inc.
; APPLICANT: Rieinger, Carl
; APPLICANT: Andersson, Maria
; APPLICANT: Lewander, Tommy
; APPLICANT: Olsson, Erik
; TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9
; FILE REFERENCE: 52459-20021.00
; CURRENT APPLICATION NUMBER: US/09/943,115A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: UK 0021286.0
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-943-115A-1

Query Match 77.3%; Score 39.4; DB 10; Length 1345;
Best Local Similarity 87.8%; Pred. No. 0.00079;
Matches 43; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 TGCTACTGGCTGCGAGCTGCAGCCCACTCTTCTTGACGACATTAACA 51
Db 1035 TGCTACTGGCTGCGAGCTGCAGCCCTGCTCTCTCTAGCATTAACA 1083

RESULT 5
US-10-146-575-3
; Sequence 3, Application US/10146575
; Publication No. US20030059800A1
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/10/146,575
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US/09/144,367
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0)...(0)
US-10-146-575-3

Query Match 77.3%; Score 39.4; DB 14; Length 1345;
Best Local Similarity 87.8%; Pred. No. 0.00079;
Matches 43; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 TGCTACTGGCTGCGAGCTGCAGCCCACTCTTCTTGACGACATTAACA 51
Db 1035 TGCTACTGGCTGCGAGCTGCAGCCCTGCTCTCTCTAGCATTAACA 1083

RESULT 6
US-10-085-612-3
; Sequence 3, Application US/10085612
; Publication No. US20030096251A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Vredenburg, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Marks, Jeffrey

;; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
;; FILE OF INVENTION: Compositions Therefor
;; FILE REFERENCE: 4389-5-C1
;; CURRENT APPLICATION NUMBER: US/10/085,612
;; CURRENT FILING DATE: 2002-02-26
;; PRIOR APPLICATION NUMBER: 09/144,367
;; PRIOR FILING DATE: 1998-08-31
;; PRIOR APPLICATION NUMBER: 60/271,630
;; PRIOR FILING DATE: 2001-02-26
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 3
;; LENGTH: 1345
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-085-612-3

Query Match 77.3%; Score 39.4; DB 14; Length 1345;
Best Local Similarity 87.8%; Pred. No. 0.00079;
Matches 43; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 TGCCTAGGCTGAGCTGACGCCCCCAGCTCTCTTCTGACGACATPAACA 51
DB 1035 TGCCTAGGCTGAGCTGACGCCCCCAGCTCTCTCTCTGACATATPAACA 1083

RESULT 7

US-10-121-960C-14
;; Sequence 14, Application US/10121960C
;; Publication No. US20030145341A1
;; GENERAL INFORMATION:
;; APPLICANT: ZHANG, Weisheng
;; APPLICANT: ZHANG, Pamela
;; APPLICANT: PURCHIO, Anthony
;; APPLICANT: HASHIMA, Sandy
;; APPLICANT: MA, Shitley
;; APPLICANT: NAMOTKA, Kevin
;; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
;; TITLE OF INVENTION: TRANSCRIPTION CONTROL ELEMENTS ASSOCIATED WITH
;; TITLE OF INVENTION: CYTOCHROME EXPRESSION
;; FILE REFERENCE: 9400-0014 / PXE-014.US
;; CURRENT APPLICATION NUMBER: US/10/121,960C
;; CURRENT FILING DATE: 2002-04-11
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 14
;; LENGTH: 13035
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: human CYP3A4 gene locus
US-10-121-960C-14

Query Match 77.3%; Score 39.4; DB 15; Length 13035;
Best Local Similarity 87.8%; Pred. No. 0.00097;
Matches 43; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 TGCCTAGGCTGAGCTGACGCCCCCAGCTCTCTTCTGACGACATPAACA 51
DB 12860 TGCCTAGGCTGAGCTGACGCCCCCAGCTCTCTCTCTGACATATPAACA 12908

RESULT 8

US-10-121-960C-17
;; Sequence 17, Application US/10121960C
;; Publication No. US20030145341A1
;; GENERAL INFORMATION:
;; APPLICANT: ZHANG, Weisheng
;; APPLICANT: ZHANG, Pamela
;; APPLICANT: PURCHIO, Anthony
;; APPLICANT: HASHIMA, Sandy
;; APPLICANT: MA, Shitley
;; APPLICANT: NAMOTKA, Kevin

;; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
;; FILE OF INVENTION: TRANSCRIPTION CONTROL ELEMENTS ASSOCIATED WITH
;; FILE REFERENCE: 9400-0014 / PXE-014.US
;; CURRENT APPLICATION NUMBER: US/10/121,960C
;; CURRENT FILING DATE: 2002-04-11
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 17
;; LENGTH: 15185
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: CYP3A4-luc transgene
US-10-121-960C-17

Query Match 77.3%; Score 39.4; DB 15; Length 15185;
Best Local Similarity 87.8%; Pred. No. 0.00098;
Matches 43; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 TGCCTAGGCTGAGCTGACGCCCCCAGCTCTCTTCTGACGACATPAACA 51
DB 12860 TGCCTAGGCTGAGCTGACGCCCCCAGCTCTCTCTCTGACATATPAACA 12908

RESULT 9

US-10-257-166-48/C
;; Sequence 48, Application US/10257166
;; Publication No. US20040023230A1
;; GENERAL INFORMATION:
;; APPLICANT: OLEK, Alexander
;; APPLICANT: PIEPENBROCK, Christian
;; APPLICANT: BERLIN, Kurt
;; TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation of
;; TITLE OF INVENTION: Genes Implicated in Pharmacogenomics
;; FILE REFERENCE: 5013.1011
;; CURRENT APPLICATION NUMBER: US/10/257,166
;; CURRENT FILING DATE: 2002-10-07
;; PRIOR APPLICATION NUMBER: PCT/EP01/07470
;; DE 10032529.7
;; DE 10043826.1
;; PRIOR FILING DATE: 2001-06-29
;; 2000-06-30
;; 2000-09-01
;; NUMBER OF SEQ ID NOS: 178
;; SEQ ID NO 48
;; LENGTH: 8943
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-257-166-48

Query Match 61.6%; Score 31.4; DB 16; Length 8943;
Best Local Similarity 77.6%; Pred. No. 0.49;
Matches 38; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 3 TGCCTAGGCTGAGCTGACGCCCCCAGCTCTTCTGACGACATPAACA 51
DB 4113 TACTACTAGTACACTGACACCTTACTCTCTCCATATPAACA 4065

RESULT 10

US-10-257-166-150/C
;; Sequence 150, Application US/10257166
;; Publication No. US20040023230A1
;; GENERAL INFORMATION:
;; APPLICANT: OLEK, Alexander
;; APPLICANT: PIEPENBROCK, Christian
;; APPLICANT: BERLIN, Kurt
;; TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation of
;; TITLE OF INVENTION: Genes Implicated in Pharmacogenomics
;; FILE REFERENCE: 5013.1011

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; CURRENT APPLICATION NUMBER: US/10/257,166
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: PCT/EP01/07470
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-06-29
; 2000-06-30
; 2000-09-01
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 150
; LENGTH: 8776
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-257-166-150

Query Match      58.4%; Score 29.8; DB 16; Length 8776;
Best Local Similarity 75.5%; Pred. No. 1.7;
Matches 37; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy      1 TTTGCTACTGGCTGCAGCTGAGCCGACCTCTTCTGCAGACATATAA 49
Db      3863 TTACTACTTAACTACACTATTAACCTTACTCTTCTCCACACATATAA 3815

RESULT 11
US-10-085-612-6
; Sequence 6, Application US/10085612
; Publication No. US20030096251A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Vredenburg, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Marks, Jeffrey
; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
; FILE REFERENCE: 4389-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-612-6

Query Match      54.9%; Score 28; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTTGCTACTGGCTGCAGCTGAGCCCA 28
Db      7 TTTGCTACTGGCTGCAGCTGAGCCCA 34

RESULT 12
US-10-775-169-80/c
; Sequence 80, Application US/10775169
; Publication No. US20040175743A1
; GENERAL INFORMATION:
; APPLICANT: Wyeeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dornier, Andrew
; APPLICANT: Trepicchio, William
```

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; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
; LENGTH: 4130
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-80

Query Match      53.3%; Score 27.2; DB 17; Length 4130;
Best Local Similarity 72.9%; Pred. No. 12;
Matches 35; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy      1 TTTGCTACTGGCTGCAGCTGAGCCGACCTCTTCTGCAGACATATA 48
Db      2148 TTAAATGCTGGCCCGCCAGCTTCAGCCCATATTAATTATCATCATCA 2101

RESULT 13
US-09-764-891-8707/c
; Sequence 8707, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8707
; LENGTH: 8575
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8707

Query Match      53.3%; Score 27.2; DB 10; Length 8575;
Best Local Similarity 72.9%; Pred. No. 13;
Matches 35; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy      1 TTTGCTACTGGCTGCAGCTGAGCCGACCTCTTCTGCAGACATATA 48
Db      6589 TTAAATGCTGGCCCGCCAGCTTCAGCCCATATTAATTATCATCATCA 6542

RESULT 14
US-10-085-612-2
; Sequence 2, Application US/10085612
; Publication No. US20030096251A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Vredenburg, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Marks, Jeffrey
; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
; FILE REFERENCE: 4389-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 34
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TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-612-2

Query Match 52.9%; Score 27; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTGCTACTGCTGCAGCTGCAGCCCC 27
DB 7 TTTGCTACTGCTGCAGCTGCAGCCCC 33

RESULT 15

US-10-425-115-176951/C
Sequence 176951, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 176951
LENGTH: 704
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_92970C.1
US-10-425-115-176951

Query Match 52.2%; Score 26.6; DB 18; Length 704;
Best Local Similarity 78.0%; Pred. No. 17;
Matches 32; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 4 GCTACTGCTGCAGCTGCAGCCCCCCTCTTCTGCAGC 44
DB 375 GCCACTGCTGCAGCTGCAGCCACCACCGCTGCAGCGGAC 335

Search completed: January 26, 2005, 19:49:31
Job time: 26.5586 secs

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